

1	TTAATTAAAGGAGGACCATC	ATG AAC GAG GCC ATC GCC GTC GTC GGC ATG TCC TGC CGC CTG CCG	64
1	M N E A I A V V G M S C R L P	15	
65	AAG GCC TCG AAC CCG GCC GCC TTC TGG GAG CTG CTG CCG AAC GGG GAG AGC GCC GTC ACC	124	
16	K A S N P A A F W E L L R N G E S A V T	35	
125	GAC GTG CCC TCC GGC CCG TGG ACG TCG GTG CTC GGG GGA GCG GAC GCC GAG GAG CCG GCG	184	
36	D V P S G R W T S V L G G A D A E E P A	55	
185	GAG TCC GGT GTC CGC CCG GGC GGC TTC CTC GAC TCC CTC GAC CTC TTC GAC GCG GCC TTC	244	
56	E S G V R R G G F L D S L D L F D A A F	75	
245	TTC GGA ATC TCG CCC CGT GAG GCC GCC GCC ATG GAC CCG CAG CAG CGA CTG GTC CTC GAA	304	
76	F G I S P R E A A A M D P Q Q Q R L V L E	95	
305	CTC GCC TGG GAG GCG CTG GAG GAC GCC GGA ATC GTC CCC GGC ACC CTC GCC GGA AGC CCG	364	
96	L A W E A L E D A G I V P G T L A G S R	115	
365	ACC GCC GTC TTC GTC GGC ACC CTG CCG GAC GAC TAC ACG AGC CTC CTC TAC CAG CAC GGC	424	
116	T A V F V G T L R D D Y T S L L Y Q H G	135	
425	GAG CAG GCC ATC ACC CAG CAC ACC ATG GCG GGC GTG AAC CCG GGC GTC ATC GCC AAC CCG	484	
136	E Q A I T Q H T M A G V N R G V I A N R	155	
485	GTC TCG TAC CAC CTC GGC CTG CAG GGC CCG AGC CTC ACC GTC GAC GCC GCG CAG TCG TCC	544	
156	V S Y H L G L Q G P S L T V D A A Q S S	175	
545	TCG CTC GTC GCC GTG CAC CTG GCC TGC GAG TCC CTG CCG GCC GGG GAG TCC ACG ACG GCG	604	
176	S L V A V H L A C E S L R A G E S T T A	195	
605	CTC GTC GCC GGC GTG AAC CTC AAC ATC CTC GCG GAG AGC GCC GTG ACG GAG GAG CCG TTC	664	
196	L V A G V N L N I L A E S A V T E E R F	215	
665	GGT GGA CTC TCC CCG GAC GGC ACC GCC TAC ACC TTC GAC GCG CCG GCC AAC GGA TTC GTC	724	
216	G G L S P D G T A Y T F D A R A N G F V	235	
725	CGG GGC GAG GGC GGC GGA GTC GTC GTA CTC AAG CCG CTC TCC CCG GCC CTC GCC GAC GGC	784	
236	R G E G G G V V V L K P L S R A L A D G	255	
785	GAC CGT GTC CAC GGC GTC ATC CCG GCC AGC GCC GTC AAC AAC GAC GGA GCC ACC CCG GGT	844	
256	D R V H G V I R A S A V N N D G A T P G	275	
845	CTC ACC GTG CCC AGC AGG GCC GCC CAG GAG AAG GTG CTG CCG GAG GCG TAC CCG AAG GCG	904	
276	L T V P S R A A Q E K V L R E A Y R K A	295	
905	GCC CTG GAC CCG TCC GCC GTC CAG TAC GTC GAA CTC CAC GGC ACC GGA ACC CCC GTC GGC	964	
296	A L D P S A V Q Y V E L H G T G T P V G	315	
965	GAC CCC ATC GAG GCC GCC GCG CTC GGC GCC GTC CTC GGC TCG GCG CCG CCC GCG GAC GAA	1024	
316	D P I E A A A L G A V L G S A R P A D E	335	
1025	CCC CTG CTC GTC GGC TCG GCC AAG ACG AAC GTC GGG CAC CTC GAA GGC GCC GCC GGC ATC	1084	
336	P L L V G S A K T N V G H L E G A A G I	355	
1085	GTC GGC CTC ATC AAG ACG CTC CTC GCG CTC GGC CCG CCG CCG ATC CCG GCG AGC CTC AAC	1144	
356	V G L I K T L L A L G R R R I P A S L N	375	
1145	TTC CGT ACG CCC CAC CCG GAC ATC CCG CTC GAC ACC CTC GGG CTC GAC GTG CCC GAC GGC	1204	
376	F R T P H P D I P L D T L G L D V P D G	395	
1205	CTG CCG GAG TGG CCG CAC CCG GAC CCG GAA CTC CTC GCC GGC GTC AGC TCG TTC GGC ATG	1264	
396	L R E W P H P D R E L L A G V S S F G M	415	
1265	GGC GGC ACC AAC GCC CAC GTC GTC CTC AGC GAA GGC CCC GCC CAG GGC GGC GAG CAG CCC	1324	
416	G G T N A H V V L S E G P A Q G G E Q P	435	
1325	GGC ATC GAT GAG GAG ACC CCC GTC GAC AGC GGC GCC GCA CTG CCC TTC GTC GTC ACC GGC	1384	
436	G I D E E T P V D S G A A L P F V V T G	455	
1385	CGC GGC GGC GAG GCC CTG CCG GCC CAG GCC CCG CCG CTG CAC GAG GCC GTC GAA GCG GAC	1444	
456	R G G E A L R A Q A R R L H E A V E A D	475	

FIG. 23A

1445	COG	GAG	CTC	GCG	CCC	GCC	GCA	CTC	GCC	CGG	TOG	CTG	GTC	ACC	ACC	CGT	ACG	GTC	TTC	ACG	1504
476	P	E	L	A	P	A	A	L	A	R	S	L	V	T	T	R	T	V	F	T	495
1505	CAC	CGG	TOG	GTC	GTC	CTC	GCC	CGG	GAC	CGC	GCC	CGC	CTC	CTC	GAC	GGC	CTC	GGC	GCC	CTC	1564
496	H	R	S	V	V	L	A	P	D	R	A	R	L	L	D	G	L	G	A	L	515
1565	GCC	GCC	GGG	ACG	CCC	GCG	CCC	GGC	GTG	GTC	ACC	GGC	ACC	CCC	GCC	CCC	GGG	CGC	CTC	GCC	1624
516	A	A	G	T	P	A	P	G	V	V	T	G	T	P	A	P	G	R	L	A	535
1625	GTC	CTG	TTC	AGC	GGC	CAG	GGT	GCC	CAA	CGT	ACG	GGC	ATG	GGC	ATG	GAG	TTC	TAC	GCC	GCC	1684
536	V	L	F	S	G	Q	G	A	Q	R	T	G	M	G	M	E	L	Y	A	A	555
1685	CAC	CCC	GCC	TTC	GCG	ACG	GCC	TTC	GAC	GCC	GTC	GCC	GCC	GAA	CTG	GAC	CCC	CTC	CTC	GAC	1744
556	H	P	A	F	A	T	A	F	D	A	V	A	A	E	L	D	P	L	L	D	575
1745	CGG	CCC	CTC	GCC	GAA	CTC	GTC	GCG	GCG	GGC	GAC	ACC	CTC	GAC	CGC	ACC	GTC	CAC	ACA	CAG	1804
576	R	P	L	A	E	L	V	A	A	G	D	T	L	D	R	T	V	H	T	Q	595
1805	CCC	GCG	CTC	TTC	GCC	GTG	GAG	GTC	GCC	CTC	CAC	CGC	CTC	GTC	GAG	TCC	TGG	GGC	GTC	ACG	1864
596	P	A	L	F	A	V	E	V	A	L	H	R	L	V	E	S	W	G	V	T	615
1865	CCC	GAC	CTG	CTC	GCC	GGC	CAC	TCC	GTC	GGC	GAG	ATC	AGC	GCC	GCC	CAC	GTC	GCC	GGG	GTC	1924
616	P	D	L	L	A	G	H	S	V	G	E	I	S	A	A	H	V	A	G	V	635
1925	CTG	TOG	CTG	CGC	GAC	GCC	GCC	CGC	CTC	GTC	GCG	GCG	CGC	GGC	CGC	CTC	ATG	CAG	GCG	CTC	1984
636	L	S	L	R	D	A	A	R	L	V	A	A	R	G	R	L	M	Q	A	L	655
1985	CCC	GAG	GGC	GGC	GCG	ATG	GTC	GCG	GTC	GAG	GCG	AGC	GAG	GAG	GAA	GTG	CTT	CCG	CAC	CTC	2044
656	P	E	G	G	A	M	V	A	V	E	A	S	E	E	E	V	L	P	H	L	675
2045	GCG	GGA	CGC	GAG	CGG	GAG	CTC	TCC	CTC	GCG	GCC	GTG	AAC	GGC	CCC	CGC	GCG	GTC	GTC	CTC	2104
676	A	G	R	E	R	E	L	S	L	A	A	V	N	G	P	R	A	V	V	L	695
2105	GCG	GGC	GCC	GAG	CGC	GCC	GTC	CTC	GAC	GTC	GCC	GAG	CTG	CTG	CGC	GAA	CAG	GGC	CGC	CGG	2164
696	A	G	A	E	R	A	V	L	D	V	A	E	L	L	R	E	Q	G	R	R	715
2165	ACG	AAG	CGG	CTC	AGC	GTC	TOG	CAC	GCC	TTC	CAC	TOG	CCG	CTC	ATG	GAG	CCG	ATG	CTC	GAC	2224
716	T	K	R	L	S	V	S	H	A	F	H	S	P	L	M	E	P	M	L	D	735
2225	GAC	TTC	CGC	CGG	GTC	GTC	GAA	GAG	CTG	GAC	TTC	CAG	GAG	CCC	CGC	GTC	GAC	GTC	GTG	TCC	2284
736	D	F	R	R	V	V	E	E	L	D	F	Q	E	P	R	V	D	V	V	S	755
2285	ACG	GTG	ACG	GGC	CTG	CCT	GTC	ACA	GCG	GGC	CAA	TGG	ACC	GAT	CCC	GAG	TAC	TGG	GTG	GAC	2344
756	T	V	T	G	L	P	V	T	A	G	Q	W	T	D	P	E	Y	W	V	D	775
2345	CAG	GTC	CGC	AGG	CCC	GTA	CGC	TTC	CTC	GAC	GCC	GTA	CGC	ACC	CTG	GAG	GAA	TOG	GGC	GCC	2404
776	Q	V	R	R	P	V	R	F	L	D	A	V	R	T	L	E	E	S	G	A	795
2405	GAC	ACC	TTC	CTG	GAG	CTC	GGT	CCC	GAC	GGG	GTC	TGC	TCC	GCG	ATG	GCG	GCG	GAC	TCC	GTA	2464
796	D	T	F	L	E	L	G	P	D	G	V	C	S	A	M	A	A	D	S	V	815
2465	CGC	GAC	CAG	GAG	GCC	GCC	ACG	GCG	GTC	TCC	GCC	CTG	CGC	AAG	GGC	CGC	CCG	GAG	CCC	CAG	2524
816	R	D	Q	E	A	A	T	A	V	S	A	L	R	K	G	R	P	E	P	Q	835
2525	TOG	CTG	CTC	GCC	GCA	CTC	ACC	ACC	GTC	TTC	GTC	CGG	GGC	CAC	GAC	GTC	GAC	TGG	ACC	GCC	2584
836	S	L	L	A	A	L	T	T	V	F	V	R	G	H	D	V	D	W	T	A	855
2585	GCG	CAC	GGG	AGC	ACC	GGC	ACG	GTC	AGG	GTG	CCC	CTG	COG	ACC	TAC	GCC	TTC	CAG	CGC	GAA	2644
856	A	H	G	S	T	G	T	V	R	V	P	L	P	T	Y	A	F	Q	R	E	875
2645	CGC	CAC	TGG	TTC	GAC	GGC	GCC	GCG	CGA	ACG	GCG	GCG	CCG	CTC	ACG	GCG	GGC	CGA	TOG	GGC	2704
876	R	H	W	F	D	G	A	A	R	T	A	A	P	L	T	A	G	R	S	G	895
2705	ACC	GGT	GCG	GGC	ACC	GGC	COG	GCC	GCG	GGT	GTG	ACG	TOG	GGC	GAG	GGC	GAG	GGC	GAG	GGC	2764
896	T	G	A	G	T	G	P	A	A	G	V	T	S	G	E	G	E	G	E	G	915
2765	GAG	GGC	GCG	GGT	GCG	GGT	GGC	GGT	GAT	CGG	CCG	GCT	CGC	CAC	GAG	ACG	ACC	GAG	CGC	GTG	2824
916	E	G	A	G	A	G	G	G	D	R	P	A	R	H	E	T	T	E	R	V	935
2825	CGC	GCA	CAC	GTC	GCC	GCC	GTC	CTC	GAG	TAC	GAC	GAC	CCG	ACC	CGC	GTC	GAA	CTC	GGC	CTC	2884
936	R	A	H	V	A	A	V	L	E	Y	D	D	P	T	R	V	E	L	G	L	955
2885	ACC	TTC	AAG	GAG	CTG	GGC	TTC	GAC	TCC	CTC	ATG	TCC	GTC	GAG	CTG	CGG	AAC	GCG	CTC	GTC	2944
956	T	F	K	E	L	G	F	D	S	L	M	S	V	E	L	R	N	A	L	V	975
2945	GAC	GAC	ACG	GGA	CTG	CGC	CTG	CCC	AGC	GGA	CTG	CTC	TTC	GAC	CAC	CCG	ACG	CCG	CGC	GCC	3004
976	D	D	T	G	L	R	L	P	S	G	L	L	F	D	H	P	T	P	R	A	995

FIG. 23B

3005	CTC	GCC	GCC	CAC	CTG	GGC	GAC	CTG	CTC	ACC	GGC	GGC	AGC	GGC	GAG	ACC	GGA	TCG	GCC	GAC	3064
996	L	A	A	H	L	G	D	L	L	T	G	G	S	G	E	T	G	S	A	D	1015
3065	GGG	ATA	CCG	CCC	GCG	ACC	CCG	GCG	GAC	ACC	ACC	GCC	GAG	CCC	ATC	GCG	ATC	ATC	GGC	ATG	3124
1016	G	I	P	P	A	T	P	A	D	T	T	A	E	P	I	A	I	I	G	M	1035
3125	GCC	TGC	CGC	TAC	CCC	GGC	GGC	GTC	ACC	TCC	CCC	GAG	GAC	CTG	TGG	CGG	CTC	GTC	GCC	GAG	3184
1036	A	C	R	Y	P	G	G	V	T	S	P	E	D	L	W	R	L	V	A	E	1055
3185	GGG	CGC	GAC	GCC	GTC	TCG	GGG	CTG	CCC	ACC	GAC	CGC	GGC	TGG	GAC	GAG	GAC	CTC	TTC	GAC	3244
1056	G	R	D	A	V	S	G	L	P	T	D	R	G	W	D	E	D	L	F	D	1075
3245	GCC	GAC	CCC	GAC	CGC	AGC	GGC	AAG	AGC	TCG	GTC	CGC	GAG	GGC	GGA	TTC	CTG	CAC	GAC	GCC	3304
1076	A	D	P	D	R	S	G	K	S	S	V	R	E	G	G	F	L	H	D	A	1095
3305	GCC	CTG	TTC	GAC	GCC	GGC	TTC	TTC	GGG	ATA	TCG	CCC	CGC	GAG	GCC	CTC	GGC	ATG	GAC	CCG	3364
1096	A	L	F	D	A	G	F	F	G	I	S	P	R	E	A	L	G	M	D	P	1115
3365	CAG	CAG	CGG	CTG	CTC	CTG	GAG	ACG	GCA	TGG	GAG	GCC	GTC	GAG	CGC	GCA	GGG	CTC	GAC	CCC	3424
1116	Q	Q	R	L	L	L	E	T	A	W	E	A	V	E	R	A	G	L	D	P	1135
3425	GAA	GGC	CTC	AAG	GGC	AGC	CGG	ACG	GCC	GTC	TTC	GTC	GGC	GCC	ACC	GCC	CTG	GAC	TAC	GGC	3484
1136	E	G	L	K	G	S	R	T	A	V	F	V	G	A	T	A	L	D	Y	G	1155
3485	CCG	CGC	ATG	CAC	GAC	GGC	GCC	GAG	GGC	GTC	GAG	GGC	CAC	CTC	CTG	ACC	GGG	ACC	ACG	CCC	3544
1156	P	R	M	H	D	G	A	E	G	V	E	G	H	L	L	T	G	T	T	P	1175
3545	AGC	GTG	ATG	TCG	GGC	CGC	ATC	GCC	TAC	CAG	CTC	GGC	CTC	ACC	GGT	CCT	GCG	GTC	ACC	GTC	3604
1176	S	V	M	S	G	R	I	A	Y	Q	L	G	L	T	G	P	A	V	T	V	1195
3605	GAC	ACG	GCC	TGC	TCG	TCC	TCG	CTC	GTC	GCG	CTG	CAC	CTG	GCC	GTC	CGT	TCG	CTG	CGG	CAG	3664
1196	D	T	A	C	S	S	S	L	V	A	L	H	L	A	V	R	S	L	R	Q	1215
3665	GGC	GAG	TCG	AGC	CTC	GCG	CTC	GCC	GGC	GGA	GCG	ACC	GTC	ATG	TCG	ACA	CCG	GGC	ATG	TTC	3724
1216	G	E	S	S	L	A	L	A	G	G	A	T	V	M	S	T	P	G	M	F	1235
3725	GTC	GAG	TTC	TCG	CGG	CAG	CGC	GGC	CTC	GCC	GCC	GAC	GGC	CGC	TCC	AAG	GCC	TTC	TCC	GAC	3784
1236	V	E	F	S	R	Q	R	G	L	A	A	D	G	R	S	K	A	F	S	D	1255
3785	TCC	GCC	GAC	GGC	ACC	TCC	TGG	GCC	GAG	GGC	GTC	GGC	CTC	CTC	GTC	GTC	GAG	CGG	CTC	TCG	3844
1256	S	A	D	G	T	S	W	A	E	G	V	G	L	L	V	V	E	R	L	S	1275
3845	GAC	GCC	GAG	CGC	AAC	GGC	CAC	CCC	GTG	CTC	GCC	GTG	ATC	CGG	GGC	AGC	GCG	GTC	AAC	CAG	3904
1276	D	A	E	R	N	G	H	P	V	L	A	V	I	R	G	S	A	V	N	Q	1295
3905	GAC	GGC	GCC	TCC	AAC	GGG	CTC	ACC	GCC	CCC	AAC	GGC	CCG	TCC	CAG	CAG	CGC	GTC	ATC	CGA	3964
1296	D	G	A	S	N	G	L	T	A	P	N	G	P	S	Q	Q	R	V	I	R	1315
3965	CAG	GCC	CTG	GCC	GAC	GCC	GGG	CTC	ACC	CCG	GCC	GAC	GTC	GAC	GCC	GTC	GAG	GCG	CAC	GGT	4024
1316	Q	A	L	A	D	A	G	L	T	P	A	D	V	D	A	V	E	A	H	G	1335
4025	ACG	GGT	ACC	CGG	CTC	GGC	GAC	CCC	ATC	GAG	GCC	GAG	GCG	ATC	CTC	GGC	ACC	TAC	GGC	CGG	4084
1336	T	G	T	R	L	G	D	P	I	E	A	E	A	I	L	G	T	Y	G	R	1355
4085	GAC	CGG	GGC	GAG	GGC	GCT	CCG	CTC	CAG	CTC	GGC	TCG	CTG	AAG	TCG	AAC	ATC	GGC	CAC	GCG	4144
1356	D	R	G	E	G	A	P	L	Q	L	G	S	L	K	S	N	I	G	H	A	1375
4145	CAG	GCC	GCC	GCG	GGC	GTG	GGC	GGG	CTC	ATC	AAG	ATG	GTC	CTC	GCG	ATG	CGC	CAC	GGC	GTC	4204
1376	Q	A	A	A	G	V	G	G	L	I	K	M	V	L	A	M	R	H	G	V	1395
4205	CTG	CCC	AGG	ACG	CTC	CAC	GTG	GAC	CGG	CCC	ACC	ACC	CGC	GTC	GAC	TGG	GAG	GCC	GGC	GGC	4264
1396	L	P	R	T	L	H	V	D	R	P	T	T	R	V	D	W	E	A	G	G	1415
4265	GTC	GAG	CTC	CTC	ACC	GAG	GAG	CGG	GAG	TGG	CCG	GAG	ACG	GGC	CGC	CCG	CGC	CGC	GCG	GCG	4324
1416	V	E	L	L	T	E	E	R	E	W	P	E	T	G	R	P	R	R	A	A	1435
4325	ATC	TCC	TCC	TTC	GGC	ATC	AGC	GGC	ACC	AAC	GCC	CAC	ATC	GTG	GTC	GAA	CAG	GCC	CCG	GAA	4384
1436	I	S	S	F	G	I	S	G	T	N	A	H	I	V	V	E	Q	A	P	E	1455
4385	GCC	GGG	GAG	GCG	GCG	GTC	ACC	ACC	ACC	GCC	CCG	GAA	GCA	GGG	GAA	GCC	GGG	GAA	GCG	GCG	4444
1456	A	G	E	A	A	V	T	T	T	A	P	E	A	G	E	A	G	E	A	A	1475
4445	GAC	ACC	ACC	GCC	ACC	ACG	ACG	CCG	GCC	GCG	GTC	GGC	GTC	CCC	GAA	CCC	GTA	CGC	GCC	CCC	4504
1476	D	T	T	A	T	T	T	P	A	A	V	G	V	P	E	P	V	R	A	P	1495
4505	GTC	GTG	GTC	TCC	GCG	CGG	GAC	GCC	GCC	GCC	CTG	CGC	GCC	CAG	GCC	GTT	CGG	CTG	CGG	ACC	4564
1496	V	V	V	S	A	R	D	A	A	A	L	R	A	Q	A	V	R	L	R	T	1515

FIG. 23C

4565	TTC	CTC	GAC	GGC	CGA	COG	GAC	GTC	ACC	GTC	GCC	GAC	CTC	GGA	CGC	TCG	CTG	GCC	GCC	CGT	4624
1516	F	L	D	G	R	P	D	V	T	V	A	D	L	G	R	S	L	A	A	R	1535
4625	ACC	GCC	TTC	GAG	CAC	AAG	GCC	GCC	CTC	ACC	ACC	GCC	ACC	AGG	GAC	GAG	CTG	CTC	GCC	GGG	4684
1536	T	A	F	E	H	K	A	A	L	T	T	A	T	R	D	E	L	L	A	G	1555
4685	CTC	GAC	GCC	CTC	GGC	CGC	GGG	GAG	CAA	GCC	ACG	GGC	CTG	GTC	ACC	GGC	GAA	CCG	GCC	AGG	4744
1556	L	D	A	L	G	R	G	E	Q	A	T	G	L	V	T	G	E	P	A	R	1575
4745	GCC	GGA	CGC	ACG	GCC	TTC	CTG	TTC	ACC	GGC	CAG	GGA	GCG	CAG	CGC	GTC	GCC	ATG	GGC	GAG	4804
1576	A	G	R	T	A	F	L	F	T	G	Q	G	A	Q	R	V	A	M	G	E	1595
4805	GAA	CTG	CGC	GCC	GCG	CAC	CCC	GTG	TTC	GCC	GCC	GCC	CTC	GAC	ACC	GTG	TAC	GCG	GCC	CTC	4864
1596	E	L	R	A	A	H	P	V	F	A	A	A	L	D	T	V	Y	A	A	L	1615
4865	GAC	CGT	CAC	CTC	GAC	CGG	CCG	CTG	CGG	GAG	ATC	GTC	GCC	GCC	GGG	GAG	GAG	CTG	GAC	CTC	4924
1616	D	R	H	L	D	R	P	L	R	E	I	V	A	A	G	E	E	L	D	L	1635
4925	ACC	GCG	TAC	ACC	CAG	CCC	GCC	CTC	TTC	GCC	TTC	GAG	GTG	GCG	CTG	TTC	CGC	CTC	CTC	GAA	4984
1636	T	A	Y	T	Q	P	A	L	F	A	F	E	V	A	L	F	R	L	L	E	1655
4985	CAC	CAC	GGC	CTC	GTC	CCC	GAC	CTG	CTC	ACC	GGC	CAC	TCC	GTG	GGC	GAG	ATC	GCC	GCC	GCG	5044
1656	H	H	G	L	V	P	D	L	L	T	G	H	S	V	G	E	I	A	A	A	1675
5045	CAC	GTC	GCC	GGT	GTC	CTC	TCC	CTC	GAC	GAC	GCC	GCA	CGT	CTC	GTC	ACC	GCC	CGC	GGC	CGG	5104
1676	H	V	A	G	V	L	S	L	D	D	A	A	R	L	V	T	A	R	G	R	1695
5105	CTC	ATG	CAG	TCG	GCC	CGC	GAG	GGC	GGC	GCG	ATG	ATC	GCC	GTG	CAG	GCG	GGC	GAG	GCC	GAG	5164
1696	L	M	Q	S	A	R	E	G	G	A	M	I	A	V	Q	A	G	E	A	E	1715
5165	GTC	GTC	GAG	TCC	CTG	AAG	GGC	TAC	GAG	GGC	AGG	GTC	GCC	GTC	GCC	GCC	GTC	AAC	GGA	CCC	5224
1716	V	V	E	S	L	K	G	Y	E	G	R	V	A	V	A	A	V	N	G	P	1735
5225	ACC	GCC	GTG	GTC	GTC	TCC	GGC	GAC	GCG	GAC	GCC	GCC	GAG	GAG	ATC	CGC	GCC	GTA	TGG	GCG	5284
1736	T	A	V	V	V	S	G	D	A	D	A	A	E	E	I	R	A	V	W	A	1755
5285	GGA	CGC	GGC	CGG	CGC	ACC	CGC	AGG	CTG	CGC	GTC	AGC	CAC	GCC	TTC	CAC	TCC	CCG	CAC	ATG	5344
1756	G	R	G	R	R	T	R	R	L	R	V	S	H	A	F	H	S	P	H	M	1775
5345	GAC	GAC	GTC	CTC	GAC	GAG	TTC	CTC	CGG	GTC	GCC	GAG	GGC	CTG	ACC	TTC	GAG	GAG	CCG	CGG	5404
1776	D	D	V	L	D	E	F	L	R	V	A	E	G	L	T	F	E	E	P	R	1795
5405	ATC	CCC	GTC	GTC	TCC	ACG	GTC	ACC	GGC	GCG	CTC	GTC	ACG	TCC	GGC	GAG	CTC	ACC	TCG	CCC	5464
1796	I	P	V	V	S	T	V	T	G	A	L	V	T	S	G	E	L	T	S	P	1815
5465	GCG	TAC	TGG	GTC	GAC	CAG	ATC	CGG	CGG	CCC	GTG	CGC	TTC	CTG	GAC	GCC	GTC	CGC	ACC	CTG	5524
1816	A	Y	W	V	D	Q	I	R	R	P	V	R	F	L	D	A	V	R	T	L	1835
5525	GCC	GCC	CAG	GAC	GCG	ACC	GTC	CTC	GTC	GAG	ATC	GGC	CCC	GAC	GCC	GTC	CTC	ACG	GCA	CTC	5584
1836	A	A	Q	D	A	T	V	L	V	E	I	G	P	D	A	V	L	T	A	L	1855
5585	GCC	GAG	GAG	GCT	CTC	GCG	CCC	GGC	ACG	GAC	GCC	COG	GAC	GCC	CGG	GAC	GTC	ACG	GTC	GTC	5644
1856	A	E	E	A	L	A	P	G	T	D	A	P	D	A	R	D	V	T	V	V	1875
5645	COG	CTG	CTG	CGC	GCG	GGG	CGC	CCC	GAG	CCC	GAG	ACC	CTC	GCC	GCC	GGT	CTC	GCG	ACC	GCC	5704
1876	P	L	L	R	A	G	R	P	E	P	E	T	L	A	A	G	L	A	T	A	1895
5705	CAT	GTC	CAC	GGC	GCA	CCC	TTG	GAC	CGG	GCG	TCG	TTC	TTC	CGG	GAC	GGG	CGC	CGC	ACG	GAC	5764
1896	H	V	H	G	A	P	L	D	R	A	S	F	F	P	D	G	R	R	T	D	1915
5765	CTG	CCC	ACG	TAC	GCC	TTC	CGG	CGC	GAG	CAC	TAC	TGG	CTG	ACG	CCC	GAG	GCC	CGT	ACG	GAC	5824
1916	L	P	T	Y	A	F	R	R	E	H	Y	W	L	T	P	E	A	R	T	D	1935
5825	GCC	CGC	GCA	CTC	GGC	TTC	GAC	COG	GCG	CGG	CAC	COG	CTG	CTG	ACG	ACC	ACG	GTC	GAG	GTC	5884
1936	A	R	A	L	G	F	D	P	A	R	H	P	L	L	T	T	T	V	E	V	1955
5885	GCC	GGC	GGC	GAC	GGC	GTC	CTG	CTG	ACC	GGC	CGT	CTC	TCC	CTG	ACC	GAC	CAG	CCC	TGG	CTG	5944
1956	A	G	G	D	G	V	L	L	T	G	R	L	S	L	T	D	Q	P	W	L	1975
5945	GCC	GAC	CAC	ATG	GTC	AAC	GGC	GCC	GTC	CTG	TTG	COG	GCC	ACC	GCC	TTC	CTG	GAG	CTC	GCC	6004
1976	A	D	H	M	V	N	G	A	V	L	L	P	A	T	A	F	L	E	L	A	1995
6005	CTC	GCG	GCG	GGC	GAC	CAC	GTC	GGG	GCG	GTC	CGG	GTG	GAG	GAA	CTC	ACC	CTC	GAA	GCG	COG	6064
1996	L	A	A	G	D	H	V	G	A	V	R	V	E	E	L	T	L	E	A	P	2015
6065	CTC	GTC	CTG	CCC	GAG	CGG	GGC	GCC	GTC	CGC	ATC	CAG	GTC	GGC	GTG	AGC	GGC	GAC	GGC	GAG	6124
2016	L	V	L	P	E	R	G	A	V	R	I	Q	V	G	V	S	G	D	G	E	2035

FIG. 23D

6125	TOG	COG	GCC	GGG	CGC	ACC	TTC	GGT	GTG	TAC	AGC	ACC	CCC	GAC	TCC	GGC	GAC	ACC	GGT	GAC	6184
2036	S	P	A	G	R	T	F	G	V	Y	S	T	P	D	S	G	D	T	G	D	2055
6185	GAC	GCG	CCC	CGG	GAG	TGG	ACC	CGC	CAT	GTC	TCC	GGC	GTA	CTC	GGC	GAA	GGG	GAC	COG	GCC	6244
2056	D	A	P	R	E	W	T	R	H	V	S	G	V	L	G	E	G	D	P	A	2075
6245	ACG	GAG	TOG	GAC	CAC	CCC	GGC	ACC	GAC	GGG	GAC	GGT	TCA	GCG	GCC	TGG	COG	CCT	GCG	GCG	6304
2076	T	E	S	D	H	P	G	T	D	G	D	G	S	A	A	W	P	P	A	A	2095
6305	GCG	ACC	GCC	ACA	CCC	CTC	GAC	GGC	GTC	TAC	GAC	CGG	CTC	GCG	GAG	CTC	GGC	TAC	GGA	TAC	6364
2096	A	T	A	T	P	L	D	G	V	Y	D	R	L	A	E	L	G	Y	G	Y	2115
6365	GGT	COG	GCC	TTC	CAG	GGC	CTG	ACG	GGG	CTG	TGG	CGC	GAC	GGC	GCC	GAC	ACG	CTC	GCC	GAG	6424
2116	G	P	A	F	Q	G	L	T	G	L	W	R	D	G	A	D	T	L	A	E	2135
6425	ATC	CGG	CTG	CCC	GCG	GCG	CAG	CAC	GAG	AGC	GCG	GGG	CTC	TTC	GGC	GTA	CAC	COG	GCG	CTG	6484
2136	I	R	L	P	A	A	Q	H	E	S	A	G	L	F	G	V	H	P	A	L	2155
6485	CTC	GAC	GCG	GCG	CTC	CAC	COG	ATC	GTC	CTG	GAG	GGC	AAC	TCA	GCT	GCC	GGT	GCC	TGT	GAC	6544
2156	L	D	A	A	L	H	P	I	V	L	E	G	N	S	A	A	G	A	C	D	2175
6545	GCC	GAT	ACC	GAC	GCG	ACC	GAC	CGG	ATC	CGG	CTG	COG	TTC	GCG	TGG	GCG	GGG	GTG	ACC	CTC	6604
2176	A	D	T	D	A	T	D	R	I	R	L	P	F	A	W	A	G	V	T	L	2195
6605	CAC	GCC	GAA	GGG	GCC	ACC	GCG	CTC	CGC	GTA	CGG	ATC	ACA	CCC	ACC	GGC	COG	GAC	ACG	GTC	6664
2196	H	A	E	G	A	T	A	L	R	V	R	I	T	P	T	G	P	D	T	V	2215
6665	ACG	CTC	CGC	CTC	ACC	GAC	ACC	ACC	GGT	GCG	CCC	GTG	GCC	ACC	GTG	GAG	TCC	CTG	ACC	CTG	6724
2216	T	L	R	L	T	D	T	T	G	A	P	V	A	T	V	E	S	L	T	L	2235
6725	CGC	GCG	GTG	GCG	AAG	GAC	CGG	CTG	GGC	ACC	ACC	GCC	GGG	CGC	GTC	GAC	GAC	GCC	CTG	TTC	6784
2236	R	A	V	A	K	D	R	L	G	T	T	A	G	R	V	D	D	A	L	F	2255
6785	ACG	GTC	GTG	TGG	ACG	GAG	ACC	GGC	ACA	COG	GAA	CCC	GCA	GGG	CGC	GGA	GCC	GTG	GAG	GTC	6844
2256	T	V	V	W	T	E	T	G	T	P	E	P	A	G	R	G	A	V	E	V	2275
6845	GAG	GAA	CTC	GTC	GAC	CTC	GCC	GGC	CTC	GGC	GAC	CTC	GTG	GAG	CTC	GGC	GCC	GCG	GAC	GTC	6904
2276	E	E	L	V	D	L	A	G	L	G	D	L	V	E	L	G	A	A	D	V	2295
6905	GTC	CTC	CGG	GCC	GAC	CGC	TGG	ACG	CTC	GAC	GGG	GAC	COG	TCC	GCC	GCC	GCG	CGC	ACA	GCC	6964
2296	V	L	R	A	D	R	W	T	L	D	G	D	P	S	A	A	A	R	T	A	2315
6965	GTC	CGG	CGC	ACC	CTC	GCC	ATC	GTC	CAG	GAG	TTC	CTG	TCC	GAG	COG	CGC	TTC	GAC	GGC	TOG	7024
2316	V	R	R	T	L	A	I	V	Q	E	F	L	S	E	P	R	F	D	G	S	2335
7025	CGA	CTG	GTG	TGC	GTC	ACC	AGG	GGC	GCG	GTC	GCC	GCA	CTC	CCC	GGC	GAG	GAC	GTC	ACC	TCC	7084
2336	R	L	V	C	V	T	R	G	A	V	A	A	L	P	G	E	D	V	T	S	2355
7085	CTC	GCC	ACC	GGC	CCC	CTC	TGG	GGC	CTC	GTC	CGC	TCC	GCC	CAG	TCC	GAG	AAC	COG	GGA	CGC	7144
2356	L	A	T	G	P	L	W	G	L	V	R	S	A	Q	S	E	N	P	G	R	2375
7145	CTG	TTC	CTC	CTG	GAC	CTG	GGT	GAA	GGC	GAA	GGC	GAG	CGC	GAC	GGA	GCC	GAG	GAG	CTG	ATC	7204
2376	L	F	L	L	D	L	G	E	G	E	G	E	R	D	G	A	E	E	L	I	2395
7205	CGC	GCG	GCC	ACG	GCC	GGG	GAC	GAG	COG	CAG	CTC	GCG	GCA	CGG	GAC	GGC	CGA	CTG	CTC	GCG	7264
2396	R	A	A	T	A	G	D	E	P	Q	L	A	A	R	D	G	R	L	L	A	2415
7265	COG	AGG	CTG	GCC	CGT	ACC	GCC	GCC	CTT	TOG	AGT	GAG	GAC	ACC	GCC	GGC	GGC	GCC	GAC	CGT	7324
2416	P	R	L	A	R	T	A	A	L	S	S	E	D	T	A	G	G	A	D	R	2435
7325	TTC	GGC	CCC	GAC	GGC	ACC	GTC	CTC	GTC	ACC	GGG	GGC	ACC	GGA	GGC	CTC	GGA	GCG	CTC	CTC	7384
2436	F	G	P	D	G	T	V	L	V	T	G	G	T	G	G	L	G	A	L	L	2455
7385	GCC	CGC	CAC	CTC	GTG	GAG	CGT	CAC	GGG	GTG	CGC	CGG	CTG	CTG	CTG	GTG	AGC	CGC	CGC	GGG	7444
2456	A	R	H	L	V	E	R	H	G	V	R	R	L	L	L	V	S	R	R	G	2475
7445	GCC	GAC	GCC	CCC	GGC	GCG	GCC	GAC	CTG	GGC	GAG	GAC	CTC	GCG	GGC	CTC	GGC	GCG	GAG	GTG	7504
2476	A	D	A	P	G	A	A	D	L	G	E	D	L	A	G	L	G	A	E	V	2495
7505	GCG	TTC	GCC	GCC	GCC	GAC	GCC	GCC	GAC	CGC	GAG	AGC	CTG	GCG	CGG	GCG	ATC	GCC	ACC	GTG	7564
2496	A	F	A	A	A	D	A	A	D	R	E	S	L	A	R	A	I	A	T	V	2515
7565	CCC	GCC	GAG	CAT	COG	CTG	ACG	GCC	GTC	GTG	CAC	ACG	GCG	GGA	GTC	GTC	GAC	GAC	GCG	ACG	7624
2516	P	A	E	H	P	L	T	A	V	V	H	T	A	G	V	V	D	D	A	T	2535
7625	GTG	GAG	GCG	CTC	ACA	COG	GAA	CGG	CTG	GAC	GCG	GTA	CTG	CGC	COG	AAG	GTC	GAC	GCC	GCG	7684
2536	V	E	A	L	T	P	E	R	L	D	A	V	L	R	P	K	V	D	A	A	2555

FIG. 23E

7685	TGG	AAC	CTG	CAC	GAG	CTC	ACC	AAG	GAC	CTG	CGG	CTC	GAC	GCC	TTC	GTC	CTC	TTC	TCC	TCC	7744
2556	W	N	L	H	E	L	T	K	D	L	R	L	D	A	F	V	L	F	S	S	2575
7745	GTC	TCC	GGC	ATC	GTC	GGC	ACC	GCC	GGC	CAG	GCC	AAC	TAC	GCG	GCG	GCC	AAC	ACG	GGC	CTC	7804
2576	V	S	G	I	V	G	T	A	G	Q	A	N	Y	A	A	A	N	T	G	L	2595
7805	GAC	GCC	CTC	GCC	GCC	CAC	CGC	GCC	GCC	ACG	GGC	CTG	GCC	GCC	ACG	TCG	CTG	GCC	TGG	GGC	7864
2596	D	A	L	A	A	H	R	A	A	T	G	L	A	A	T	S	L	A	W	G	2615
7865	CTC	TGG	GAC	GGC	ACG	CAC	GGC	ATG	GGC	GGC	ACG	CTC	GGC	GCC	GCC	GAC	CTC	GCC	CGC	TGG	7924
2616	L	W	D	G	T	H	G	M	G	G	T	L	G	A	A	D	L	A	R	W	2635
7925	AGC	CGG	GCC	GGA	ATC	ACC	CCG	CTC	ACC	CCG	CTG	CAG	GGC	CTC	GCG	CTC	TTC	GAC	GCC	GCG	7984
2636	S	R	A	G	I	T	P	L	T	P	L	Q	G	L	A	L	F	D	A	A	2655
7985	GTC	GCC	AGG	GAC	GAC	GCC	CTC	CTC	GTA	CCC	GCC	GGG	CTC	CGT	CCC	ACC	GCC	CAC	CGG	GGC	8044
2656	V	A	R	D	D	A	L	L	V	P	A	G	L	R	P	T	A	H	R	G	2675
8045	ACG	GAC	GGA	CAG	CCT	CCT	GCG	CTG	TGG	CGC	GGC	CTC	GTC	CGG	GCG	CGC	CCG	CGC	CGT	GCC	8104
2676	T	D	G	Q	P	P	A	L	W	R	G	L	V	R	A	R	P	R	R	A	2695
8105	GCG	CGG	ACG	GCC	GCC	GAG	GCG	GCG	GAC	ACG	ACC	GGC	GGC	TGG	CTG	AGC	GGG	CTC	GCC	GCA	8164
2696	A	R	T	A	A	E	A	A	D	T	T	G	G	W	L	S	G	L	A	A	2715
8165	CAG	TCC	CCC	GAG	GAG	CGG	CGC	AGC	ACA	GCC	GTC	ACG	CTC	GTG	ACG	GGT	GTC	GTC	GCG	GAC	8224
2716	Q	S	P	E	E	R	R	S	T	A	V	T	L	V	T	G	V	V	A	D	2735
8225	GTC	CTC	GGG	CAC	GCC	GAC	TCC	GCC	GCG	GTC	GGG	GCG	GAG	CGG	TCC	TTC	AAG	GAC	CTC	GGC	8284
2736	V	L	G	H	A	D	S	A	A	V	G	A	E	R	S	F	K	D	L	G	2755
8285	TTC	GAC	TCC	CTG	GCC	GGG	GTG	GAG	CTC	CGC	AAC	CGG	CTG	AAC	GCC	GCC	ACC	GGC	CTG	CGG	8344
2756	F	D	S	L	A	G	V	E	L	R	N	R	L	N	A	A	T	G	L	R	2775
8345	CTC	CCC	GCG	ACC	ACG	GTC	TTC	GAC	CAT	CCC	TOG	CCG	GCC	GCG	CTC	GCG	TCC	CAT	CTC	CTC	8404
2776	L	P	A	T	T	V	F	D	H	P	S	P	A	A	L	A	S	H	L	L	2795
8405	GCC	CAG	GTG	CCC	GGG	TTG	AAG	GAG	GGG	ACG	GCG	GCG	ACC	GCG	ACC	GTC	GTG	GCC	GAG	CGG	8464
2796	A	Q	V	P	G	L	K	E	G	T	A	A	T	A	T	V	V	A	E	R	2815
8465	GGC	GCT	TCC	TTC	GGT	GAC	CGT	GCG	ACC	GAC	GAC	GAT	CCG	ATC	GCG	ATC	GTG	GGC	ATG	GCA	8524
2816	G	A	S	F	G	D	R	A	T	D	D	D	P	I	A	I	V	G	M	A	2835
8525	TGC	CGC	TAT	CCG	GGT	GGT	GTG	TCG	TOG	CCG	GAG	GAC	CTG	TGG	CGG	CTG	GTG	GCC	GAG	GGG	8584
2836	C	R	Y	P	G	G	V	S	S	P	E	D	L	W	R	L	V	A	E	G	2855
8585	ACG	GAC	GCG	ATC	AGC	GAG	TTC	CCC	GTC	AAC	CGC	GGC	TGG	GAC	CTG	GAG	AGC	CTC	TAC	GAC	8644
2856	T	D	A	I	S	E	F	P	V	N	R	G	W	D	L	E	S	L	Y	D	2875
8645	CCG	GAT	CCC	GAG	TCG	AAG	GGC	ACC	ACG	TAC	TGC	CGG	GAG	GGC	GGG	TTC	CTG	GAA	GGC	GCC	8704
2876	P	D	P	E	S	K	G	T	T	Y	C	R	E	G	G	F	L	E	G	A	2895
8705	GGT	GAC	TTC	GAC	GCC	GCC	TTC	TTC	GGC	ATC	TOG	CCG	CGC	GAG	GCC	CTG	GTG	ATG	GAC	CCG	8764
2896	G	D	F	D	A	A	F	F	G	I	S	P	R	E	A	L	V	M	D	P	2915
8765	CAG	CAG	CGG	CTG	CTG	CTG	GAG	GTG	TCC	TGG	GAG	GCG	CTG	GAA	CGC	GCG	GGC	ATC	GAC	CCG	8824
2916	Q	Q	R	L	L	L	E	V	S	W	E	A	L	E	R	A	G	I	D	P	2935
8825	TCC	TCG	CTG	CGC	GGC	AGC	CGC	GGT	GGT	GTC	TAC	GTG	GGC	GCC	GCG	CAC	GGC	TCG	TAC	GCC	8884
2936	S	S	L	R	G	S	R	G	G	V	Y	V	G	A	A	H	G	S	Y	A	2955
8885	TCC	GAT	CCC	CGG	CTG	GTG	CCC	GAG	GGC	TCG	GAG	GGC	TAT	CTG	CTG	ACC	GGC	AGC	GCC	GAC	8944
2956	S	D	P	R	L	V	P	E	G	S	E	G	Y	L	L	T	G	S	A	D	2975
8945	GCG	GTG	ATG	TCC	GGC	CGC	ATC	TCC	TAC	GCG	CTC	GGT	CTC	GAA	GGA	CCG	TCC	ATG	ACG	GTG	9004
2976	A	V	M	S	G	R	I	S	Y	A	L	G	L	E	G	P	S	M	T	V	2995
9005	GAG	ACG	GCC	TGC	TCC	TCC	TCG	CTG	GTG	GCG	CTG	CAT	CTG	GCG	GTA	CGG	GCG	CTG	CGG	CAC	9064
2996	E	T	A	C	S	S	S	L	V	A	L	H	L	A	V	R	A	L	R	H	3015
9065	GGC	GAG	TGC	GGG	CTC	GCG	CTG	GCG	GGC	GGG	GTG	GCG	GTG	ATG	GCC	GAT	CCG	GCG	GCG	TTC	9124
3016	G	E	C	G	L	A	L	A	G	G	V	A	V	M	A	D	P	A	A	F	3035
9125	GTG	GAG	TTC	TCC	CGG	CAG	AAG	GGG	CTG	GCC	GCC	GAC	GGC	CGC	TGC	AAG	GCG	TTC	TCG	GCC	9184
3036	V	E	F	S	R	Q	K	G	L	A	A	D	G	R	C	K	A	F	S	A	3055
9185	GCC	GCC	GAC	GGC	ACC	GGC	TGG	GCC	GAG	GGC	GTC	GGC	GTG	CTC	GTC	CTG	GAG	CGG	CTG	TCG	9244
3056	A	A	D	G	T	G	W	A	E	G	V	G	V	L	V	L	E	R	L	S	3075

FIG. 23F

9245	GAC	GCG	CGC	CGC	GCG	GGG	CAC	ACG	GTC	CTC	GGC	CTG	GTC	ACC	GGC	ACC	GCG	GTC	AAC	CAG	9304
3076	D	A	R	R	A	G	H	T	V	L	G	L	V	T	G	T	A	V	N	Q	3095
9305	GAC	GGT	GCC	TCC	AAC	GGG	CTG	ACC	GCG	CCC	AAC	GGC	CCA	GCC	CAG	CAA	CGC	GTC	ATC	GCC	9364
3096	D	G	A	S	N	G	L	T	A	P	N	G	P	A	Q	Q	R	V	I	A	3115
9365	GAG	GCG	CTC	GCC	GAC	GCC	GGG	CTG	TCC	CCG	GAG	GAC	GTG	GAC	GCG	GTC	GAG	GCG	CAC	GGC	9424
3116	E	A	L	A	D	A	G	L	S	P	E	D	V	D	A	V	E	A	H	G	3135
9425	ACC	GGC	ACC	CGG	CTC	GGC	GAC	CCC	ATC	GAG	GCC	GGG	GCG	CTG	CTC	GCC	GCC	TCC	GGA	CGG	9484
3136	T	G	T	R	L	G	D	P	I	E	A	G	A	L	L	A	A	S	G	R	3155
9485	AAC	CGT	TCC	GGC	GAC	CAC	CCG	CTG	TGG	CTC	GGC	TCG	CTG	AAG	TCC	AAC	ATC	GGG	CAT	GCC	9544
3156	N	R	S	G	D	H	P	L	W	L	G	S	L	K	S	N	I	G	H	A	3175
9545	CAG	GCC	GCC	GCC	GGT	GTC	GGC	GGC	GTC	ATC	AAG	ATG	CTC	CAG	GCG	CTG	CGG	CAC	GGC	TTG	9604
3176	Q	A	A	A	G	V	G	G	V	I	K	M	L	Q	A	L	R	H	G	L	3195
9605	CTG	CCC	CGC	ACC	CTC	CAC	GCC	GAC	GAG	COG	ACC	CCG	CAT	GCC	GAC	TGG	AGC	TCC	GGC	CGG	9664
3196	L	P	R	T	L	H	A	D	E	P	T	P	H	A	D	W	S	S	G	R	3215
9665	GTA	CGG	CTG	CTC	ACC	TCC	GAG	GTG	CCG	TGG	CAG	CGG	ACC	GGC	CGG	CCC	CGG	CGG	ACC	GGG	9724
3216	V	R	L	L	T	S	E	V	P	W	Q	R	T	G	R	P	R	R	T	G	3235
9725	GTG	TCC	GCC	TTC	GGC	GTC	GGC	GGC	ACC	AAT	GCC	CAT	GTC	GTC	CTC	GAA	GAG	GCA	CCC	GCC	9784
3236	V	S	A	F	G	V	G	G	T	N	A	H	V	V	L	E	E	A	P	A	3255
9785	CCG	CCC	GCG	CCG	GAA	CCG	GCC	GGG	GAG	GCC	CCC	GGC	GGC	TCC	CGC	GCC	GCA	GAA	GGG	GCG	9844
3256	P	P	A	P	E	P	A	G	E	A	P	G	G	S	R	A	A	E	G	A	3275
9845	GAA	GGG	CCC	CTG	GCC	TGG	GTG	GTC	TCC	GGA	CGC	GAC	GAG	CCG	GCC	CTG	CGG	TCC	CAG	GCC	9904
3276	E	G	P	L	A	W	V	V	S	G	R	D	E	P	A	L	R	S	Q	A	3295
9905	CGG	CGG	CTC	CGC	GAC	CAC	CTC	TCC	CGC	ACC	CCC	GGG	GCC	CGC	CCG	CGT	GAC	ATC	GCC	TTC	9964
3296	R	R	L	R	D	H	L	S	R	T	P	G	A	R	P	R	D	I	A	F	3315
9965	TCC	CTC	GCC	GCC	ACG	CGC	GCA	GCC	TTT	GAC	CAC	CGC	GCC	GTG	CTG	ATC	GGC	TCG	GAC	GGG	10024
3316	S	L	A	A	T	R	A	A	F	D	H	R	A	V	L	I	G	S	D	G	3335
10025	GCC	GAA	CTC	GCC	GCC	GCC	CTG	GAC	GCG	TTG	GCC	GAA	GGA	CGC	GAC	GGT	CCG	GCG	GTG	GTG	10084
3336	A	E	L	A	A	A	L	D	A	L	A	E	G	R	D	G	P	A	V	V	3355
10085	CGC	GGA	GTC	CGC	GAC	CGG	GAC	GGC	AGG	ATG	GCC	TTC	CTC	TTC	ACC	GGG	CAG	GGC	AGC	CAG	10144
3356	R	G	V	R	D	R	D	G	R	M	A	F	L	F	T	G	Q	G	S	Q	3375
10145	CGC	GCC	GGG	ATG	GCC	CAC	GAC	CTG	CAT	GCC	GCC	CAT	ACC	TTC	TTC	GCG	TCC	GCC	CTC	GAC	10204
3376	R	A	G	M	A	H	D	L	H	A	A	H	T	F	F	A	S	A	L	D	3395
10205	GAG	GTG	ACG	GAC	CGT	CTC	GAC	COG	CTG	CTC	GGC	CGG	COG	CTC	GGC	GCG	CTG	CTG	GAC	GCC	10264
3396	E	V	T	D	R	L	D	P	L	L	G	R	P	L	G	A	L	L	D	A	3415
10265	CGA	CCC	GGC	TCG	CCC	GAA	GCG	GCA	CTC	CTG	GAC	CGG	ACC	GAG	TAC	ACC	CAG	CCG	GCG	CTC	10324
3416	R	P	G	S	P	E	A	A	L	L	D	R	T	E	Y	T	Q	P	A	L	3435
10325	TTC	GCC	GTC	GAG	GTG	GCG	CTC	CAC	CGG	CTG	CTG	GAG	CAC	TGG	GGG	ATG	CGC	CCC	GAC	CTG	10384
3436	F	A	V	E	V	A	L	H	R	L	L	E	H	W	G	M	R	P	D	L	3455
10385	CTG	CTG	GGG	CAC	TCG	GTG	GGC	GAA	CTG	GCG	GCC	GCC	CAC	GTC	GCG	GGT	GTG	CTC	GAT	CTC	10444
3456	L	L	G	H	S	V	G	E	L	A	A	A	H	V	A	G	V	L	D	L	3475
10445	CAC	GAC	GCC	TGC	GCG	CTG	GTG	GCC	GCC	CGC	GGC	AGG	CTG	ATG	CAG	CGC	CTG	CCG	CCC	GGC	10504
3476	D	D	A	C	A	L	V	A	A	R	G	R	L	M	Q	R	L	P	P	G	3495
10505	GGC	GCG	ATG	GTC	TCC	GTG	CGG	GCC	GGC	GAG	GAC	GAG	GTC	CGC	GCA	CTG	CTG	GCC	GGC	CGC	10564
3496	G	A	M	V	S	V	R	A	G	E	D	E	V	R	A	L	L	A	G	R	3515
10565	GAG	GAC	GCC	GTC	TGC	GTC	GCC	GCG	GTG	AAC	GGC	CCC	CGG	TCG	GTG	GTG	ATC	TCC	GGC	GCG	10624
3516	E	D	A	V	C	V	A	A	V	N	G	P	R	S	V	V	I	S	G	A	3535
10625	GAG	GAA	GCG	GTG	GCC	GAG	GCG	GCG	GCG	CAG	CTC	GCC	GGA	CGA	GGC	CGC	CGC	ACC	AGG	CGG	10684
3536	E	E	A	V	A	E	A	A	A	Q	L	A	G	R	G	R	R	T	R	R	3555
10685	CTC	CGC	GTC	GCG	CAC	GCC	TTC	CAC	TCA	CCC	CTG	ATG	GAC	GGC	ATG	CTC	GCC	GGA	TTC	CGG	10744
3556	L	R	V	A	H	A	F	H	S	P	L	M	D	G	M	L	A	G	F	R	3575
10745	GAG	GTC	GCC	GCC	GGC	CTG	CGC	TAC	CGG	GAA	CCG	GAG	CTG	ACG	GTC	GTC	TCC	ACG	GTC	ACG	10804
3576	E	V	A	A	G	L	R	Y	R	E	P	E	L	T	V	V	S	T	V	T	3595

FIG. 23G

10805	GGG	CGG	CCC	GCC	CGC	CCC	GGT	GAA	CTC	ACC	GGC	CCC	GAC	TAC	TGG	GTG	GCC	CAG	GTC	CGT	10864
3596	G	R	P	A	R	P	G	E	L	T	G	P	D	Y	W	V	A	Q	V	R	3615
10865	GAG	CCC	GTG	CGC	TTC	GCG	GAC	GCG	GTC	CGC	ACG	GCA	CAC	CGC	CTC	GGA	GCC	CGC	ACC	TTC	10924
3616	E	P	V	R	F	A	D	A	V	R	T	A	H	R	L	G	A	R	T	F	3635
10925	CTG	GAG	ACC	GGC	CCG	GAC	GGC	GTG	CTG	TGC	GGC	ATG	GCA	GAG	GAG	TGC	CTG	GAG	GAC	GAC	10984
3636	L	E	T	G	P	D	G	V	L	C	G	M	A	E	E	C	L	E	D	D	3655
10985	ACC	GTG	GCC	CTG	CTG	CCG	GCG	ATC	CAC	AAG	CCC	GGC	ACC	GCG	CCG	CAC	GGT	CCG	GCG	GCT	11044
3656	T	V	A	L	L	P	A	I	H	K	P	G	T	A	P	H	G	P	A	A	3675
11045	CCC	GGC	GCG	CTG	CGG	GCG	GCC	GCC	GCC	GCG	TAC	GGC	CGG	GGC	GCC	CGG	GTG	GAC	TGG	GCC	11104
3676	P	G	A	L	R	A	A	A	A	A	Y	G	R	G	A	R	V	D	W	A	3695
11105	GGG	ATG	CAC	GCC	GAC	GGC	CCC	GAG	GGG	CCG	GCC	CGC	CGC	GTC	GAA	CTG	CCC	GTC	CAC	GCC	11164
3696	G	M	H	A	D	G	P	E	G	P	A	R	R	V	E	L	P	V	H	A	3715
11165	TTC	CGG	CAC	CGC	CGC	TAC	TGG	CTC	GCC	CCG	GGC	CGC	GCG	GCG	GAC	ACC	GAC	GAC	TGG	ATG	11224
3716	F	R	H	R	R	Y	W	L	A	P	G	R	A	A	D	T	D	D	W	M	3735
11225	TAC	CGG	ATC	GGC	TGG	GAC	CGG	CTG	CCG	GCT	GTG	ACC	GGC	GGG	GCC	CGG	ACC	GCC	GGC	CGC	11284
3736	Y	R	I	G	W	D	R	L	P	A	V	T	G	G	A	R	T	A	G	R	3755
11285	TGG	CTG	GTG	ATC	CAC	CCC	GAC	AGC	CCG	CGC	TGC	CGG	GAG	CTG	TCC	GGC	CAC	GCC	GAA	CGC	11344
3756	W	L	V	I	H	P	D	S	P	R	C	R	E	L	S	G	H	A	E	R	3775
11345	GCG	CTG	CGC	GCC	GCG	GGC	GCG	AGC	CCC	GTA	CCG	CTG	CCC	GTG	GAC	GCT	CCG	GCC	GCC	GAC	11404
3776	A	L	R	A	A	G	A	S	P	V	P	L	P	V	D	A	P	A	A	D	3795
11405	CGG	GCG	TCC	TTC	GCG	GCA	CTG	CTG	CGC	TCC	GCC	ACC	GGA	CCT	GAC	ACA	CGA	GGT	GAC	ACA	11464
3796	R	A	S	F	A	A	L	L	R	S	A	T	G	P	D	T	R	G	D	T	3815
11465	GCC	GCG	CCC	GTG	GCC	GGT	GTG	CTG	TGG	CTG	CTG	TCC	GAG	GAG	GAT	CGG	CCC	CAT	CGC	CAG	11524
3816	A	A	P	V	A	G	V	L	S	L	L	S	E	E	D	R	P	H	R	Q	3835
11525	CAC	GCC	CCG	GTA	CCC	GCC	GGG	GTC	CTG	GCG	ACG	CTG	TCC	CTG	ATG	CAG	GCT	ATG	GAG	GAG	11584
3836	H	A	P	V	P	A	G	V	L	A	T	L	S	L	M	Q	A	M	E	E	3855
11585	GAG	GCG	GTG	GAG	GCT	CGC	GTG	TGG	TGC	GTC	TCC	CGC	GCC	GCG	GTC	GCC	GCC	GCC	GAC	CGG	11644
3856	E	A	V	E	A	R	V	W	C	V	S	R	A	A	V	A	A	A	D	R	3875
11645	GAA	CGG	CCC	GTC	GGC	GCG	GGC	GCC	GCC	CTG	TGG	GGG	CTG	GGG	CGG	GTG	GCC	GCC	CTG	GAA	11704
3876	E	R	P	V	G	A	G	A	A	L	W	G	L	G	R	V	A	A	L	E	3895
11705	CGC	CCC	ACC	CGG	TGG	GGC	GGT	CTC	GTG	GAC	CTG	CCC	GCC	TGG	CCC	GGT	GCG	GCG	CAC	TGG	11764
3896	R	P	T	R	W	G	G	L	V	D	L	P	A	S	P	G	A	A	H	W	3915
11765	GCG	GCC	GCC	GTG	GAA	CGG	CTC	GCC	GGT	CCC	GAG	GAC	CAG	ATC	GCC	GTG	CGC	GCG	TCC	GGC	11824
3916	A	A	A	V	E	R	L	A	G	P	E	D	Q	I	A	V	R	A	S	G	3935
11825	AGT	TGG	GGC	CGG	CGC	CTC	ACC	AGG	CTG	CCG	CGC	GAC	GGC	GGC	GGC	CGG	ACG	GCC	GCA	CCC	11884
3936	S	W	G	R	R	L	T	R	L	P	R	D	G	G	G	R	T	A	A	P	3955
11885	GCG	TAC	CGG	CCG	CGC	GGC	ACG	GTG	CTC	GTC	ACC	GGT	GGC	ACC	GGC	GCG	CTC	GGC	GGG	CAT	11944
3956	A	Y	R	P	R	G	T	V	L	V	T	G	G	T	G	A	L	G	G	H	3975
11945	CTC	GCC	CGC	TGG	CTC	GCC	GCG	GCG	GGC	GAA	CAC	CTG	GCG	CTC	ACC	AGC	CGC	CGG	GGC		12004
3976	L	A	R	W	L	A	A	A	G	A	E	H	L	A	L	T	S	R	R	G	3995
12005	CCG	GAC	GCG	CCC	GGC	GCC	GCC	GGA	CTC	GAG	GCC	GAA	CTC	CTC	CTC	CTG	GCC	GCC	AAG	GTG	12064
3996	P	D	A	P	G	A	A	G	L	E	A	E	L	L	L	L	G	A	K	V	4015
12065	ACG	TTC	GCC	GCC	TGC	GAC	ACC	GCC	GAC	CGC	GAC	GGC	CTC	GCC	CGG	GTC	CTG	CGG	GCG	ATA	12124
4016	T	F	A	A	C	D	T	A	D	R	D	G	L	A	R	V	L	R	A	I	4035
12125	CCG	GAG	GAC	ACC	CCG	CTC	ACC	GCG	GTG	TTC	CAC	GCC	GCG	GGC	GTA	CCG	CAG	GTC	ACG	CCG	12184
4036	P	E	D	T	P	L	T	A	V	F	H	A	A	G	V	P	Q	V	T	P	4055
12185	CTG	TCC	CGT	ACC	TGG	CCC	GAG	CAC	TTC	GCC	GAC	GTG	TAC	GCG	GGC	AAG	GCG	GCG	GGC	GCC	12244
4056	L	S	R	T	S	P	E	H	F	A	D	V	Y	A	G	K	A	A	G	A	4075
12245	GCG	CAC	CTG	GAC	GAA	CTG	ACC	CGC	GAA	CTC	GGC	GCC	GGA	CTC	GAC	GCG	TTC	GTC	CTC	TAC	12304
4076	A	H	L	D	E	L	T	R	E	L	G	A	G	L	D	A	F	V	L	Y	4095
12305	TCC	TCC	GGC	GCC	GGC	GTC	TGG	GGC	AGC	GCC	GGC	CAG	GGT	GCC	TAC	GCC	GCC	GCC	AAC	GCC	12364
4096	S	S	G	A	G	V	W	G	S	A	G	Q	G	A	Y	A	A	A	N	A	4115

FIG. 23H

12365	GCC	CTG	GAC	GCG	CTC	GCC	CGG	CGC	CGT	GCG	GCG	GAC	GGA	CTC	CCC	GCC	ACC	TCC	ATC	GCC	12424
4116	A	L	D	A	L	A	R	R	R	A	A	D	G	L	P	A	T	S	I	A	4135
12425	TGG	GGC	GTG	TGG	GGC	GGC	GGT	ATG	GGG	GCC	GAC	GAG	GCG	GGC	GCG	GAG	TAT	CTG	GGC	12484	
4136	W	G	V	W	G	G	G	M	G	A	D	E	A	G	A	E	Y	L	G	4155	
12485	CGG	CGC	GGT	ATG	CGC	CCC	ATG	GCA	CCG	GTC	TCC	GCG	CTC	CGG	GCG	ATG	GCC	ACC	GCC	ATC	12544
4156	R	R	G	M	R	P	M	A	P	V	S	A	L	R	A	M	A	T	A	I	4175
12545	GCC	TCC	GGG	GAA	CCC	TGC	CCC	ACC	GTC	ACC	CAC	ACC	GAC	TGG	GAG	CGC	TTC	GGC	GAG	GGC	12604
4176	A	S	G	E	P	C	P	T	V	T	H	T	D	W	E	R	F	G	E	G	4195
12605	TTC	ACC	GCC	TTC	CGG	CCC	AGC	CCT	CTG	ATC	GCG	GGG	CTC	GGC	ACG	CCG	GGC	GGC	GGC	CGG	12664
4196	F	T	A	F	R	P	S	P	L	I	A	G	L	G	T	P	G	G	G	R	4215
12665	GCG	GCG	GAG	ACC	CCC	GAG	GAG	GGG	AAC	GCC	ACC	GCT	GCG	GCG	GAC	CTC	ACC	GCC	CTG	CCG	12724
4216	A	A	E	T	P	E	E	G	N	A	T	A	A	A	D	L	T	A	L	P	4235
12725	CCC	GCC	GAA	CTC	CGC	ACC	GCG	CTG	CGC	GAG	CTG	GTG	CGA	GCC	CGG	ACC	GCC	GCG	GCG	CTC	12784
4236	P	A	E	L	R	T	A	L	R	E	L	V	R	A	R	T	A	A	A	L	4255
12785	GGC	CTC	GAC	GAC	CCG	GCC	GAG	GTC	GCC	GAG	GGC	GAA	CGG	TTC	CCC	GCC	ATG	GGC	TTC	GAC	12844
4256	G	L	D	D	P	A	E	V	A	E	G	E	R	F	P	A	M	G	F	D	4275
12845	TCC	CTG	GCC	ACC	GTA	CGG	CTG	CGC	CGC	GGA	CTC	GCC	TCG	GCC	ACG	GGC	CTC	GAC	CTG	CCC	12904
4276	S	L	A	T	V	R	L	R	R	G	L	A	S	A	T	G	L	D	L	P	4295
12905	CCC	GAT	CTG	CTC	TTC	GAC	CGG	GAC	ACC	CCG	GCC	GCG	CTC	GCC	GCC	CAC	CTG	GCC	GAA	CTG	12964
4296	P	D	L	L	F	D	R	D	T	P	A	A	L	A	A	H	L	A	E	L	4315
12965	CTC	GCC	ACC	GCA	CGG	GAC	CAC	GGA	CCC	GGC	GGC	CCC	GGG	ACC	GGT	GCC	GCG	CCG	GCC	GAT	13024
4316	L	A	T	A	R	D	H	G	P	G	G	P	G	T	G	A	A	P	A	D	4335
13025	GCC	GGA	AGC	GGC	CTG	CCG	GCC	CTC	TAC	CGG	GAG	GCC	GTC	CGC	ACC	GGC	CGG	GCC	GCG	GAA	13084
4336	A	G	S	G	L	P	A	L	Y	R	E	A	V	R	T	G	R	A	A	E	4355
13085	ATG	GCC	GAA	CTG	CTC	GCC	GCC	GCT	TCC	CGG	TTC	CGC	CCC	GCC	TTC	GGG	ACG	GCG	GAC	CGG	13144
4356	M	A	E	L	L	A	A	A	S	R	F	R	P	A	F	G	T	A	D	R	4375
13145	CAG	CCG	GTG	GCC	CTC	GTG	CCG	CTG	GCC	GAC	GGC	GCG	GAG	GAC	ACC	GGG	CTC	CCG	CTG	CTC	13204
4376	Q	P	V	A	L	V	P	L	A	D	G	A	E	D	T	G	L	P	L	L	4395
13205	GTG	GGC	TGC	GCC	GGG	ACG	GCG	GTG	GCC	TCC	GGC	CCG	GTG	GAG	TTC	ACC	GCC	TTC	GCC	GGA	13264
4396	V	G	C	A	G	T	A	V	A	S	G	P	V	E	F	T	A	F	A	G	4415
13265	GCG	CTG	GCG	GAC	CTC	CCG	GCG	GCG	GCC	CCG	ATG	GCC	GCG	CTG	CCG	CAG	CCC	GGC	TTC	CTG	13324
4416	A	L	A	D	L	P	A	A	A	P	M	A	A	L	P	Q	P	G	F	L	4435
13325	CCG	GGA	GAA	CGA	GTC	CCG	GCC	ACC	CCG	GAG	GCA	TTG	TTC	GAG	GCC	CAG	GCG	GAA	GCG	CTG	13384
4436	P	G	E	R	V	P	A	T	P	E	A	L	F	E	A	Q	A	E	A	L	4455
13385	CTG	CGC	TAC	GCG	GCC	GGC	CGG	CCC	TTC	GTG	CTG	CTG	GGG	CAC	TCC	GCC	GGC	GCC	AAC	ATG	13444
4456	L	R	Y	A	A	G	R	P	F	V	L	L	G	H	S	A	G	A	N	M	4475
13445	GCC	CAC	GCC	CTG	ACC	CGT	CAT	CTG	GAG	GCG	AAC	GGT	GGC	GGC	CCC	GCA	GGG	CTG	GTG	CTC	13504
4476	A	H	A	L	T	R	H	L	E	A	N	G	G	G	P	A	G	L	V	L	4495
13505	ATG	GAC	ATC	TAC	ACC	CCC	GCC	GAC	CCC	GGC	GCG	ATG	GGC	GTC	TGG	CGG	AAC	GAC	ATG	TTC	13564
4496	M	D	I	Y	T	P	A	D	P	G	A	M	G	V	W	R	N	D	M	F	4515
13565	CAG	TGC	GTC	TGG	CGG	CGC	TCG	GAC	ATC	CCC	CCG	GAC	GAC	CAC	CGC	CTC	ACG	GCC	ATG	GGC	13624
4516	Q	W	V	W	R	R	S	D	I	P	P	D	D	H	R	L	T	A	M	G	4535
13625	GCC	TAC	CAC	CGG	CTG	CTT	CTC	GAC	TGG	TCG	CCC	ACC	CCC	GTC	CGC	GCC	CCC	GTA	CTG	CAT	13684
4536	A	Y	H	R	L	L	L	D	W	S	P	T	P	V	R	A	P	V	L	H	4555
13685	CTG	CGC	GCC	GCG	GAA	CCC	ATG	GGC	GAC	TGG	CCA	CCC	GGG	GAC	ACC	GGC	TGG	CAG	TCC	CAC	13744
4556	L	R	A	A	E	P	M	G	D	W	P	P	G	D	T	G	W	Q	S	H	4575
13745	TGG	GAC	GGC	GCG	CAC	ACC	ACC	GCC	GGC	ATC	CCC	GGA	AAC	CAC	TTC	ACG	ATG	ATG	ACC	GAA	13804
4576	W	D	G	A	H	T	T	A	G	I	P	G	N	H	F	T	M	M	T	E	4595
13805	CAC	GCC	TCC	GCC	GCC	GCC	CGG	CTC	GTG	CAC	GGC	TGG	CTC	GCG	GAA	CGG	ACC	CCG	TCC	GGG	13864
4596	H	A	S	A	A	A	R	L	V	H	G	W	L	A	E	R	T	P	S	G	4615
13865	CAG	GGC	GGG	TCA	CCG	TCC	CGC	GCG	GCG	GGG	AGA	GAG	GAG	AGG	CCG	TGA	ACACGGCAGCCGGCCCC			13928	
4616	Q	G	G	S	P	S	R	A	A	G	R	E	E	R	P	*					4631

FIG. 231

13929 GACCGGCACCGCGCGCGCGCGGCACCAACCGCCCCGCGCGCGGCACACGACCTGTCCCGCGCGCGGAACGAGGCTCCAACCTCA 14008

14009 CCCGGGCGGCACAGTGGTTTCGCGCGCAACCCAGGGAGACCCCTACGGG ATG ATC CTG CGC GCC GGC ACC GCC 14079
1 M I L R A G T A 8

14080 GAC CCG GCA CCG TAC GAG GAA GAG ATC CCC GGG TAC CGA GCT CGA ATT CTT AAT TAA GGAG 14140
9 D P A P Y E E E I P G Y R A R I L N * 27

14141 GTCGTAG ATG AGT AAC AAG AAC AAC GAT GAG CTG CAG CGG CAG GCC TCG GAA AAC ACC CTG 14201
1 M S N K N N D E L Q R Q A S E N T L 18

14202 GGG CTG AAC CCG GTC ATC GGT ATC CGC CGC AAA GAC CTG TTG AGC TCG GCA CGC ACC GTG 14261
19 G L N P V I G I R R K D L L S S A R T V 38

14262 CTG CGC CAG GCC GTG CGC CAA CCG CTG CAC AGC GCC AAG CAT GTG GCC CAC TTT GGC CTG 14321
39 L R Q A V R Q P L H S A K H V A H F G L 58

14322 GAG CTG AAG AAC GTG CTG CTG GGC AAG TCC AGC CTT GCC CCG GAA AGC GAC GAC CGT CGC 14381
59 E L K N V L L G K S S L A P E S D D R R 78

14382 TTC AAT GAC CCG GCA TGG AGC AAC AAC CCA CTT TAC CGC CGC TAC CTG CAA ACC TAT CTG 14441
79 F N D P A W S N N P L Y R R Y L Q T Y L 98

14442 GCC TGG CGC AAG GAG CTG CAG GAC TGG ATC GGC AAC AGC GAC CTG TCG CCC CAG GAC ATC 14501
99 A W R K E L Q D W I G N S D L S P Q D I 118

14502 AGC CGC GGC CAG TTC GTC ATC AAC CTG ATG ACC GAA GCC ATG GCT CCG ACC AAC ACC CTG 14561
119 S R G Q F V I N L M T E A M A P T N T L 138

14562 TCC AAC CCG GCA GCA GTC AAA CGC TTC TTC GAA ACC GGC GGC AAG AGC CTG CTC GAT GGC 14621
139 S N P A A V K R F F E T G G K S L L D G 158

14622 CTG TCC AAC CTG GCC AAG GAC CTG GTC AAC AAC GGT GGC ATG CCC AGC CAG GTG AAC ATG 14681
159 L S N L A K D L V N N G G M P S Q V N M 178

14682 GAC GCC TTC GAG GTG GGC AAG AAC CTG GGC ACC AGT GAA GGC GCC GTG GTG TAC CGC AAC 14741
179 D A F E V G K N L G T S E G A V V Y R N 198

14742 GAT GTG CTG GAG CTG ATC CAG TAC AAG CCC ATC ACC GAG CAG GTG CAT GCC CGC CCG CTG 14801
199 D V L E L I Q Y K P I T E Q V H A R P L 218

14802 CTG GTG GTG CCG CCG CAG ATC AAC AAG TTC TAC GTA TTC GAC CTG AGC CCG GAA AAG AGC 14861
219 L V V P P Q I N K F Y V F D L S P E K S 238

14862 CTG GCA CGC TAC TGC CTG CGC TCG CAG CAG CAG ACC TTC ATC ATC AGC TGG CGC AAC CCG 14921
239 L A R Y C L R S Q Q Q T F I I S W R N P 258

14922 ACC AAA GCC CAG CGC GAA TGG GGC CTG TCC ACC TAC ATC GAC GCG CTC AAG GAG GCG GTC 14981
259 T K A Q R E W G L S T Y I D A L K E A V 278

14982 GAC GCG GTG CTG GCG ATT ACC GGC AGC AAG GAC CTG AAC ATG CTC GGT GCC TGC TCC GGC 15041
279 D A V L A I T G S K D L N M L G A C S G 298

15042 GGC ATC ACC TGC ACG GCA TTG GTC GGC CAC TAT GCC GCC CTC GGC GAA AAC AAG GTC AAT 15101
299 G I T C T A L V G H Y A A L G E N K V N 318

15102 GCC CTG ACC CTG CTG GTC AGC GTG CTG GAC ACC ACC ATG GAC AAC CAG GTC GCC CTG TTC 15161
319 A L T L L V S V L D T T M D N Q V A L F 338

15162 GTC GAC GAG CAG ACT TTG GAG GCC GCC AAG CGC CAC TCC TAC CAG GCC GGT GTG CTC GAA 15221
339 V D E Q T L E A A K R H S Y Q A G V L E 358

15222 GGC AGC GAG ATG GCC AAG GTG TTC GCC TGG ATG CGC CCC AAC GAC CTG ATC TGG AAC TAC 15281
359 G S E M A K V F A W M R P N D L I W N Y 378

15282 TGG GTC AAC AAC TAC CTG CTC GGC AAC GAG CCG CCG GTG TTC GAC ATC CTG TTC TGG AAC 15341
379 W V N N Y L L G N E P P V F D I L F W N 398

15342 AAC GAC ACC ACG CGC CTG CCG GCC GCC TTC CAC GGC GAC CTG ATC GAA ATG TTC AAG AGC 15401
399 N D T T R L P A A F H G D L I E M F K S 418

15402 AAC CCG CTG ACC CGC CCG GAC GCC CTG GAG GTT TGC GGC ACT CCG ATC GAC CTG AAA CAG 15461
419 N P L T R P D A L E V C G T P I D L K Q 438

15462 GTC AAA TGC GAC ATC TAC AGC CTT GCC GGC ACC AAC GAC CAC ATC ACC CCG TGG CAG TCA 15521
439 V K C D I Y S L A G T N D H I T P W Q S 458

FIG. 23J

15522	TGC	TAC	CGC	TCG	GCG	CAC	CTG	TTC	GGC	GGC	AAG	ATC	GAG	TTC	GTG	CTG	TCC	AAC	AGC	GGC	15581
459	C	Y	R	S	A	H	L	F	G	G	K	I	E	F	V	L	S	N	S	G	478
15582	CAC	ATC	CAG	AGC	ATC	CTC	AAC	CCG	CCA	GGC	AAC	CCC	AAG	GCG	CGC	TTC	ATG	ACC	GGT	GCC	15641
479	H	I	Q	S	I	L	N	P	P	G	N	P	K	A	R	F	M	T	G	A	498
15642	GAT	CGC	CCG	GGT	GAC	CCG	GTG	GCC	TGG	CAG	GAA	AAC	GCC	ACC	AAG	CAT	GCC	GAC	TCC	TGG	15701
499	D	R	P	G	D	P	V	A	W	Q	E	N	A	T	K	H	A	D	S	W	518
15702	TGG	CTG	CAC	TGG	CAA	AGC	TGG	CTG	GGC	GAG	CGT	GCC	GGC	GAG	CTG	GAA	AAG	GCG	CCG	ACC	15761
519	W	L	H	W	Q	S	W	L	G	E	R	A	G	E	L	E	K	A	P	T	538
15762	CGC	CTG	GGC	AAC	CGT	GCC	TAT	GCC	GCT	GGC	GAG	GCA	TCC	CCG	GGC	ACC	TAC	GTT	CAC	GAG	15821
539	R	L	G	N	R	A	Y	A	A	G	E	A	S	P	G	T	Y	V	H	E	558
15822	CGT	TGA	GCTGCAGCGCCGTTGGCCACCTGCGGGACGCCACGGTGTGAATTTC																	15872	
559	R	*																		560	

FIG. 23K

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
BamHI									
▼									
GGATCCGACC	GTGGGTGTGA	ATCTCCGGGT	GCTCGCCTCG	TCTTGCCCG	TTACCTGTCC	GCCTCCCGCT	CCAGACCAGC	GGGAGGCGGA	CAGGGGCATG
100									
SphI									
▼									
CCGCGCGGCG	GGCTAACGGC	CGGTGCGGCG	TCCGTACGAC	GAGCCTCGCG	CGCCCTGGCG	GCCCTTGGTC	TGCCGGACCT	GTGCGCGGGG	TGCGCAGGCT
200									
BstXI									
▼									
TGCGCGCGCG	GCCTGGGCGC	GTATCTGCGG	CTCCCGGGCA	CGGCGGCGCT	GTCTGTCTCC	GAGTCATAGT	CCCTGCGCGC	GGCGCCACCG	CCCTGGGCGCG
300									
SphI									
▼									
GCATCGCGCT	GCCTGGGCGC	CCCGGCGCGT	AAGTCGCGCT	GGAGGCGCTG	AAAAGGCGGA	TCCATTTGGT	GAGCGTGAGG	TCCCTTGGCA	GTCCGCGCGTC
400									
EcoRI									
ApoI									
▼									
CGGATTTCCG	TGGCGGTCCG	CGAGGGAACG	GTAGTCCCG	TGCGGATGT	GGGCGCGGAG	GATCTCCCG	AGGCCCGGTC	CGGGGCGGCT	GAAGACGGCT
500									

FIG. 31A

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

TCCGCGAAGT TCTGGGAAGC GCGGCTCGCG CTCTCGGGCA GCAGGGGCTG GGGCGGTCCG CTGATCTCA GGACGCGCC GTCCAGCGG GGCATCGGAC 600

GGAACGACGA GCGCGGAGC CGGTCTGCGA CCGCGAATC GTACCAGGG GCCCAGGAG TCGTGAGGAG CGATCCGCG CTGCGACCG CCGGTTTGGC 700

GGCGACCTCC CACTGCACCTA TCAGGGCGCG CGACTGCGAG TTGCTCGATT CCAGGAGACT CCGGAGAATC TGGTCTGTA TGCCGAAGG AACGTTTCCG 800

ACGACGGTGT CGATATCGCG CGGAATGCGG AAGTCGAGGA AATCACCCTG GAATACGGTG ACCCTCTCC CTTCGAATTT CCGCGGCACA TGCGGGGGCC 900

AGTCGGGGTC CATCTCCACG ACCGTACCG TGTGGAAGGA GCGCACCAAC TCTCTGGTGA TCGCGCCCTT TCGGGGGCG ATTTCGAGAA CGTTCTTACC 1000

EcoRV BsmI Apol
▼ ▼ ▼
BstBI

FIG. 31B

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GTCCCCCTCG ACATGCGTGA CGAGATWGG CACGGCTCTG TCGTCTGGA GGAAGTCTTG GCCTAATTCG CCGCGAAGGG TGTGCGGTC CGCTCGACTC 1100

GGTATGGAGT CGAGCATATGC CATgaacgat cccctccctg gatgccgtgg tcaatggact tggcacggac catacctcac ggtccgtcgg acgaccggag 1200

XmnI



aagaagtcca cgcacgggcg ttccggagta cgggagttgt gaacggccgc gacgaagtgc gtcgcggttc ggcggggcgt gacgagcgag gtccggagga 1300

acgcgacgaa gcagccgaac cccaagtgcg gtgcgacgga gtgacattgg gggcatacgg agggttgtcg tacggagcgc actcaacgag gctccaggag 1400

ggaggggttg aaccgcgcgc cgactggcct tcgccgcccg cgcggccgga gtagtgcatag tcgggggtga aatcaagcca ttccccccggg atcgggtgtt 1500

FIG. 31C

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plPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

accatccct ttacctggcg tggatttccc aaccttggt atagagcgg agacgacgc acaccatgga gaccacgcac accacgagcg ccaccccccg 1600

gccatccga caaggggggt ccggtcgcc tcccgacacc catggcctgg ggtacacgcc aggtatagg ggaacgtagg gggagcatag ggggggtgccc 1700

ctggggttgg gtgaaagcgc ggcttccgga gacgggagccg gatgtcttca gccggaatta ccaggaccgg tgcgagaaca ccggtgacag ggcgtggggc 1800
 M S S A G I T R T G A R T P V T G R G A

ggcagcgtgg gacacggggg aagtgcgggt ccgacggggg ttgccccctg ccggccccga tcatgaggag cactccttct ctctgtctcc taccggtgat 1900
 A A W D T G E V R V R R G L P P A G P D H A E H S F S R A P T G D

EcoRI
 ApeI

XmnI

gtcggcgccg aattgattcg tggagagatg tcgacagtgt ccaagagtga gtccgaggaa ttctgtgtccg tgtcgaaaga cgcgggttcc ggcacggcca 2000
 V R A E L I R G E M S T V S K S E S E E F V S V S N D A G S A H G T

FIG. 31D

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pikPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CAGCGGAACC CGTGGCCGTC GTCGGCATCT CCTGCCGGGT GCCCGGGCC CGGACCCGA GAGAGTTCTG GGAATCCTG GCGGCAGGCG GCCAGGCCGT 2100
A E P V A V V G I S C R V P G A R D P R E F W E L L A A G G Q A V

CACCGACGTC CCCGGGACC GCTGGAGCG CGGGACTTC TAGACCCGG ACGCTCCGC CCCGGCCGC TCGAACAGCC GGTGGGCGG GTTCATCGAG 2200
T D V P A D R W N A G D F Y D P D R S A P G R S N S R W G G F I E

GACGTCGACC GGTTCGACGC CGCCTTCTTC GGCATCTCGC CCCGGAGGC CGCGGAGATG GACCCGACG AGCGGCTCGC CCTGGAGCTG GGCTGGGAGG 2300
D V D R F D A A F F G I S P R E A A E M D P Q Q R L A L E L G W E A

CCCTGGAGCG CGCGGGATC GACCGGTCCT CGCTCACC GGCTCTTCG CGGGGCCAT CTGGGACGAC TACGCCACCC TGAAGCACCG 2400
L E R A G I D P S S L T G T R T G V F A G A I W D D Y A T L K H R

CCAGGGGGC GCCGGGATCA CCCCGCACAC CGTCACCGGC CTCACCGCG GCATCATCGC GAACCGACTC TCGTACACGC TCGGGCTCGG CGGCCCCAGC 2500
Q G G A A I T P H T V T G L H R G I I A N R L S Y T L G L R G P S

FIG. 31E

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

ATGTCGTGCG ACTCCGGCCA GTCTCTGTCG CTCGTGCGCG TCCACCTCGC GTGCGAGAGC CTGCGGGCGG GCGAGTCCGA GCTCGCCCTC GCCGGCGCGG 2600
 M V V D S G Q S S S L V A V H L A C E S L R R G E S E L A L A G G V

TCTCGCTCAA CCTGTGTGCG GACAGCATCA TCGGGGGGAG CAAGTTCCGC GGCCTCTCCC CCGACGGCGG CCGCTACACC TTCGACGCGC GCGCCACCGG 2700
 S L N L V P D S I I G A S K F G G L S P D G R A Y T F D A R A N G

SnaBI



CTACGTACGC GCGGAGGGCG GCGGTTCGT CGTCTGTAAG CGCCTCTCCC GGGCGTCCG CCGGTGCTCG CCGTATCCG GGGCAGCGCC 2800
 Y V R G E G G G F V V L K R L S R A V A D G D P V L A V I R G S A

GTCAACAACG GCGGCGCCGC CCAGGGCATG ACGACCCCGG ACGGCGAGGC GTGCTCCGCG AGGCCACCGA GCGGGCCGGG ACCGCGCGCG 2900
 V N N G G A A Q G M T T P D A Q A Q E A V L R E A H E R A G T A P A

CCGACGTGCG GTACGTGCGG CTGCACGGCA CCGGCACCCC CGTGGGGGAC CCGATCGAGG CCGTGGCGCT CCGGCGCGCC CTCGGCACCG GCCGCCCGGC 3000
 D V R Y V E L H G T G T P V G D P I E A A A L G A A L G T G R P A

FIG. 31F

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CGGACAGCCG	CTCCTGGTGG	GCTCGGTCAA	GACGAACATC	GGCCACCTGG	AGGGCGCGGC	CGGCATCGCC	GGCCTCATCA	AGGCCGTCCT	GGCGGTCCGC
3100	G Q P	L L V G	S V K T	N I G H L E	G A A G I A	G L I K	A V L A	V R	
GGTCGGCGGC	TGCCCGCCAG	CCTGAACTAC	GAGACCCCGA	ACCCGGCGAT	CCCGTTCGAG	GAACCTGAACC	TCCGGGTGAA	CACGGAGTAC	CTGCCGTGGG
3200	G R A L	P A S L	N Y E T P N	P A I P F E	E L N L	R V N T	E Y L P	W E	
AGCCGGAGCA	CGACGGGCAG	CGGATGGTGG	TCGGCGTGTC	CTCGTTCGGC	ATGGCGGGCA	CGAACCGGCA	TGTCGTGCTC	GAAGAGGCC	CCGGGGGTGG
3300	P E H D	G Q R M V V	G V S S F G	M G G T N A	H V V L	E E A P	G G C		
TCGAGGTGCT	TCGTCGTGG	AGTCGACGGT	CGGCGGGTGG	GCGTCGGCG	GCGGTGTGGT	GCCGTGGGTG	GTGTCGGCGA	AGTCCGCTGC	CGCGCTGGAC
3400	R G A S	V V E S T V	G G S A V G	G G V V P W	V V S A	K S A A	A L D		
GCGCAGATCG	AGCGGCTTGC	CGCGTTCCGC	TCGCGGGATC	GTACGGATGG	TGTCGACGCG	GGCGTGTGCG	ATGCGGGTGC	TGTCGATGCG	GGTGTGTGCG
3500	A Q I E	R L A A F A	S R D R T D	G V D A G A	V D A G A	V D A G A	V A		

FIG. 31G

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CTCGCGTACT	GGCGGGCGGG	CGTGCTCAGT	TCGAGCACCG	GGCGGTCTGTC	GTCGGCAGCG	GGCGGACGCA	TCTGGGCGCA	GGCGTGGCGG	CGCCTGAGGG
R V L	A G G	R A Q F	E H R	A V V	V G S G	P D D	L A A	A L A	A P E G
TCTGGTCCGG	GGCGTGGCTT	CCGGTGTCCG	GCGAGTGGCG	TTGGTGTTC	CCGGGCAGGG	CACGCAGTGG	GCCGGCATGG	GTGCCGAACT	GCTGGACTCT
L V R	G V A S	G V G	R V A	F V F	P G Q G	T Q W	A G M G	A E L	L D S
BsmI									
TCGCGGTGT	TCGCGGGCGC	CATGGCCGAA	TGCGAGGCGG	CACCTCTCCC	GTACGTGAC	TGGTGGCTGG	AGGCCGTGCT	ACGGCAGGCG	CCCGGTGCGC
S A V	F A A A	M A E	C E A A	L S P	Y V D	W S L E	A V V	R Q A	P G A P
CCACGCTGGA	GGGGTTCGAT	GTCGTGCAGC	CTGTGACGTT	CGCGTTCATG	GTCTCGCTGG	CTCGCGTGTG	GCAGCACCCAC	GGGGTGACGC	CCCAGGCGGT
T L E	R V D	V V Q	P V T	F A V	M V S	L A R	V W Q	H H G	V T P Q A V
CGTCGGCCAC	TCGCAGGGCG	AGATCGCCGC	CGCGTACGTC	GCCGGTGCCC	TGAGCCTGGA	CGACGCGGCT	CGTGTCTGTA	CCCTGGCGAG	CAAGTCCATC
V G H	S Q G E	I A A	A Y V	A G A	L S L D	D A A	R V V	T L R S	K S I

FIG. 31H

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pikPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GGCGCCACC TCGCCGGCAA GCGCGGCATG CTGTCCCTCG CGCTGAGCGA GGACGCCGTC CTGGAGCGAC TGGCCGGGTT CGACGGGCTG TCCGTGCGCG 4100									
A A H L A G K G G M L S L A L S E D A V L E R L A G F D G L S V A A									
CTGTGAACGG GCCACACGCC ACCGTGGTCT CCGGTGACCC CGTACAGATC GAAGAGCTTG CTCGGGCGTG TGAGGCCGAT GGGGTCCGTG CGCGGGTCAT 4200									
V N G P T A T V V S G D P V Q I E E L A R A C E A D G V R A R V I									
TCCCCTCGAC TACCGTCCC ACAGCCGGCA GGTGAGATC ATCGAGAGCG AGCTCGCGA GGTCTCGCC GGGCTCAGCC CGCAGGTCC GCGCGTCCG 4300									
P V D Y A S H S R Q V E I I E S E L A E V L A G L S P Q A P R V P									
TTCTTCTCGA CACTCGAAGG CGCCTGGATC ACCGAGCCCG TGCTCGACGG CGGCTACTGG TACCGCAACC TCGGCCATCG TGTGGGCTTC GCCCGGCGCG 4400									
P F S T L E G A W I T E P V L D G G Y W Y R N L R H R V G F A P A V									
TCGAGACCC TGGCCACCGAC GAGGCTTCA CCGACTTCGT CGAGGTGAGC GCCACCCCG TCCTCACCAT GGCCCTCCCC GGGACCGTCA CCGGTCTGGC 4500									
E T L A T D E G F T H F V E V S A H P V L T M A L P G T V T G L A									

FIG. 311

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
MaeI									
BfaI									
▼									
GACCTGCGT	CGCGACAACG	GCGGTACAGG	CGGCCTAGTC	GCCTCCCTCG	CCGAAGCATG	GGCCAACGGA	CTCGCGGTCTG	ACTGGAGCCC	GCTCCTCCCC
4600									
T L R	R D N G	G Q D	R L V	A S L A	E A W	A N G	L A V D	W S P	L L P
MluI									
▼									
TCCGCGACG	GCCACCACTC	CGACCTCCCC	ACCTACGCGT	TCCAGACCGA	GCGCCACTGG	CTGGGCGAGA	TCGAGGCGCT	CGCCCCGCGG	GGCGAGCCGG
4700									
S A T G	H H S	D L P	T Y A F	Q T E	R H W	L G E I	E A L	A P A	G E P A
CGGTGAGCC	CGCCGTCTC	CGCACGGAGG	CGGCGAGCTC	GACCGGACG	AGCAGCTGCG	CGTGATCCTG	GACAAGGTCC	GGGCGCAGAC	4800
V Q P	A V L	R T E A	A E P A	E L D	R D E	Q L R	V I L	D K V	R A Q T
GGCCCAGGTG	CTGGGGTACG	CGACAGGCGG	GCAGATCGAG	GTCGACCGGA	CCTTCCGTGA	GGCGGGTTGC	ACCTCCCTGA	CCGGCGTGGA	CCTGCGCAAC
4900									
A Q V	L G Y A	T G G	Q I E	V D R	T F R E	A G C	T S L	T G V D	L R N
ApaLI									
▼									
CGGATCAACG	CCGCCTTCGG	CGTACGGATG	GCGCCGTCCA	TGATCTTCGA	CTTCCCCACC	CCGAGGCTC	TCGCGGAGCA	GCTGCTCCTC	GTCGTGCACG
5000									
R I N A	A F G	V R M	A P S M	I F D	F P T	P E A	L A E	Q L L	L V H G

FIG. 31J

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GGGAGGCGGC GGCAGAACCG GCCGGTGCGG AGCCGGCTCC GGTGGCGGCG GCCGGTGCCG TCGACGAGCC GGTGGCGATC GTCGGCATGG CCTGCCGCCT 5100
E A A A N P A G A E P A P V A A A G A V D E P V A I V G M A C R L

GCCCGGTGGG GTCGCCTCGC CGGAGGACCT GTGGCGGCTG GTGGCCGGCG GCGGGGACGC GATCTCGGAG TTCCCGCAGG ACCGCGGCTG GGACGTGGAG 5200
P G G V A S P E D L W R L V A G G G D A I S E F P Q D R G W D V E

BamHI
▼

GGGCTGTACC ACCCGATCC GGAGCACCCC GGCACGTCGT ACGTCGCCCA GGGCGGTTTC ATCGAGAACG TCGCCGGCTT CGACGCGGCC TTCTTCGGGA 5300
G L Y H P D P E H P G T S Y V R Q G G F I E N V A G F D A A F F G I

TCTCGCCGCG CGAGGCGCTC GCCATGGACC CGCAGCAGCG GCTCCTCCTC GAAACCTCCT GGGAGGCCGT CGAGGACGCC GGGATCGACC CGACCTCCCT 5400
S P R E A L A M D P Q Q R L L L L E T S W E A V E D A G I D P T S L

GCGGGGACGG CAGGTCGGCG TCTTCACTGG GCGATGACC CACGAGTACG GGCCGAGCCT GCGGGACGCC GGGGAAGGCC TCGACGGCTA CCTGCTGACC 5500
R G R Q V G V F T G A M T H E Y G P S L R D G G E G L D G Y L L T

FIG. 31K

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GGCAACACGG CCAGCGTGAT GTCGGGCCGC GTCTCGTACA CACTCGGCCT TGAGGGCCCC GCCCTGACGG TGGACACGGC CTGCTCGTCG TCGTGTGTCG 5600
 G N T A S V M S G R V S Y T L G L E G P A L T V D T A C S S S L V A

CCCTGCACCT CGCCGTGCAG GCCCTGGCGA AGGGCGAGGT CGACATGGCG CTCGGCGCG GCGTGGCCGT GATGCCACCG CCGGGATGT TCGTCGAGTT 5700
 L H L A V Q A L R K G E V D M A L A G G V A V M P T P G M F V E F

XmnI



CAGCCGGCAG CGCGGGCTGG CCGGCGACGG CCGGTCGAAG GCGTTCGCCG CGTCGGCGGA CGGCACCAGC TGGTCCGAGG GCGTCGGCGT CCTCCTCGTC 5800
 S R Q R G L A G D G R S K A F A A S A D G T S W S E G V G V L L V

GAGCGCCTGT CGGACGCCCC CGGCAACGGA CACCAGGTCC TCGCGGTGCT CGCGGCGCAG GCCTTGAACC AGGACGGCGC GAGCAACGGC CTCACGGCTC 5900
 E R L S D A R R N G H Q V L A V V R G S A L N Q D G A S N G L T A P

CGAACGGGCC CTCGCAGCAG CGCGTCATCC GCGCGCGGCT GCGGACGCC CGGCTGACGA CCTCCGACGT GGAGTCGTC GAGGCACAG GCACGGGCAC 6000
 N G P S Q Q R V I R R A L A D A R L T T S D V D V V E A H G T G T

FIG. 31L

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GGGACTCGGC	GACCCGATCG	AGGCGCAGGC	CCTGATCGCC	ACCTACGGCC	AGGCGCGTGA	CGACGAACAG	CCGCTGCGCC	TCGGGTGCGT	GAGTCCAAAC
R L G	D P I E	A Q A	L I A	T Y G Q	G R D	D E Q	P L R L	G S L	K S N
6100									
ATCGGGCACA	CCGAGGCCGC	GGCCGGCGTC	TCCGGTGTCA	TCAAGATGGT	CCAGCGGATG	CGCCACGGAC	TGCTGCCGAA	GACGCTGCAC	GTCGACGAGC
I G H T	Q A A	A G V	S G V I	K M V	Q A M	R H G L	L P K	T L H	V D E P
6200									
CCTCGGACCA	GATCGACTGG	TCGGCTGGCG	CCGTGGAAC	CCTCACCAG	GCCGTCGACT	GGCCGGAGAA	GCAGGACGGC	GGGCTGCGCC	GGGCGCGCGT
S D Q	I D W	S A G A	V E L	L T E	A V D W	P E K	Q D G	G L R R	A A V
6300									
CTCCTCCTTC	GGGATCAGCG	GCACCAATGC	GCATGTGTG	CTCGAAGAGG	CCCGGTGGT	TGTCGAGGCT	GCTTCGGTGC	TCGAGCCGTC	GGTTGGCGGG
S S F	G I S G	T N A	H V V	L E E A	P V V	V E G	A S V V	E P S	V G G
6400									
TCGGCGGTTC	GCGGCGGTGT	GACGCTTGG	GTGGTGTGG	CGAAGTCCGC	TGCCGCGCTC	GACGCGCAGA	TCGAGCGGCT	TGCCGATTC	GCCTCGCGGG
S A V G	G G V	T P W	V V S A	K S A	A A L	D A Q I	E R L	A A F	A S R D
6500									

BamI



FIG. 31M

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
ATCGTACGGA	TGACGCCGAC	GCCGGTCTG	TCGACGCGG	CGCTGTCGCT	CACGTACTGG	CTGACGGGG	TGCTCAGTTC	GAGCACCGG	CCGTGCGGCT
R T D D A D	A G A V D A G	A V A H V L A	D G R A Q F	E H R A V A	L				
6600									
GGCGCCGGG	GCGACGACC	TCGTACAGG	GCTGGCGAT	CCGACGGGC	TGATACGGG	AACGGCTTC	GGTGTGGGC	GAGTGGCGTT	CGTGTTCCTC
G A G A D D L	V Q A L A D	P D G L I R G	T A S G V G R	V A F V F P					
6700									
3GTCAGGGCA	CGCAGTGGC	TGGCATGGT	GCCGAACCTGC	TGACTCTTC	CGCGGTGTC	GCGGGGCCA	TGGCCGAGTG	TGAGGCCCGG	CTGTCCCGCT
3 Q G T Q W A	G M G A E L L	D S S A V F A	A A M A E C E	A A L S P Y					
6800									
ACGTGCACTG	GTGCTGGAG	GCCGTGCTAC	GCCAGGCCCC	CGGTGCGCC	ACGCTGGAGC	GGTCTGATGT	CGTGCAGCCT	GTGACGTTTCG	CCGTCAATGGT
V D W S L E	A V V R Q A P	Q A P G A P	T L E R V D V	V Q P V T F A	V M V				
6900									
CTCGCTGGCT	CGCGTGTGG	AGCACCACG	TGTGACGCCC	CAGGCGGTTCG	TCGGCCACTC	GCAGGGCGAG	ATCGCGCGC	CGTACGTGCG	CGGAGCCCTG
S L A R V W Q	H H G V T P	Q A V V G H S	Q G E I A A A	Y V A G A L					
7000									

FIG. 31N

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

SphI
▼

CCCCTGGACG ACGCCGCCCG CGTCGTACAC CTGCGCAGCA AGTCCATCGC CGCCACCTC GCGGCAAGG GCGGCATGCT GTCCCTCGCG CTGAACGAGG 7100
P L D D A A R V V T L R S K S I A A H L A G K G G M L S L A L N E D

ACGCCGTCTT GGAGCGACTG AGTGACTTCG ACGGGCTGTC CGTCGCCGCC GTCAACGGGC CCACGCCAC TGTGCTGTCG GGTGACCCCG TACAGATCGA 7200
A V L E R L S D F D G L S V A A V N G P T A T V V S G D P V Q I E

MluI
▼

AGAGCTTGCT CAGGCGTGCA AGGCGGACGG ATTCCGCGCG CGGATCATTG CCGTCGACTA CGGTCGCCAC AGCCGGCAGG TCGAGATCAT CGAGAGCGAG 7300
E L A Q A C K A D G F R A R I I P V D Y A S H S R Q V E I I E S E

CTCGCCGAGG TCCTGCGCGG TCTCAGCCCG CAGGCCCGCG GCGTCCGCTT CTTCCTGACG CTCGAAGGCA CCTGGATCAC CGAGCCCGTC CTCGACGGCA 7400
L A Q V L A G L S P Q A P R V P F F S T L E G T W I T E P V L D G T

KpnI
▼
Acc65I
▼

CCTACTGGTA CCGCAACCTC CGTCACCGCG TCGGCTTCGG CCGGCCATC GAGACCCCTGG CCGTCGACGA GGGCTTCACG CACTTCGTCG AGGTCAGCGC 7500
Y W Y R N L R H R V G F A P A I E T L A V D E G F T H F V E V S A

FIG. 310

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pkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CCACCCCGTC CTCACCATGA CCTTCCCCGA GACCGTCACC GGCCTCGSCA CCTCCGTCG CGAACAGGGA GGCCNAGAGC GTCTGGTCAC CTGCTCGCC 7600
H P V L T M T L P E T V T G L G T L R R E Q G G Q E R L V T S L A

Eco47III
▼

GAGCGTGGG TCAACGGGCT TCCGTTGGCA TGGACTTCGC TCCTGCCGCG CACGGCCTCC CGCCCGGTC TGCCACCTA CGCCTTCCAG GCCGAGCGCT 7700
E A W V N G L P V A W T S L L P A T A S R P G L P T Y A F Q A E R Y

XhoI
PaeR7I
▼

MscI
Bali
▼

ACTGGCTCGA GAACACTCCC GCCGCCCTGG CCACCGGCGA CGACTGGCGC TACCGCATCG ACTGGAAGCG CCTCCCGGCC GCCGAGGGGT CCGAGCGCAC 7800
W L E N T P A A L A T G D D W R Y R I D W X R L P A A E G S E R T

CGGCTGTCC GGCCGCTGGC TCGCCGTCAC GCGGAGGAC CACTCCGCGC AGGCCGCGC CGTGTCTACC GCGTGGTCG ACGCCGGGC GAAGGTCGAG 7900
G L S G R W L A V T P E D H S A Q A A A V L T A L V D A G A K V E

GTGCTGACGG CCGGGGCGGA CGACGACCGT GAGGCCCTCG CCGCCCGGCT CACCGCACTG ACGACGGTG ACGGCTTAC CGGCGTGGT TCGCTCCTCG 8000
V L T A G A D D D R E A L A A R L T A L T T G D G F T G V V S L L D

FIG. 31P

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pkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

ACGGACTCGT ACCGACAGTC GCCTGGGTCC AGCGCTCTCGG CGACGCCCGGA ATCAAGGCGC CCTGTGGTC CGTACCCAG GCGCGGTCT CCGTCGGACG 8100
G L V P Q V A W V Q A L G D A G I K A P L W S V T Q G A V S V G R

TCTCGACACC CCGGCCGACC CCGACCGGC CATGCTCTGG GGCCTCGGC GGTCTGTCG CCTGAGCAC CCGAACGCT GGGCCGGCCT CGTCGACCTC 8200
L D T P A D P D R A M L W G L G R V V A L E H P E R W A G L V D L

BsaBI
▼

CCGCCCCAGC CCGATGCGC CGCCTCGCC CACTCTGTCA CCGCACTTC CCGCGCCACC GCGAGGACC AGATCGCCAT CCGCACCACC GGACTCCACG 8300
P A Q P D A A A L A H L V T A L S G A T G E D Q I A I R T T G L H A

CCGCGCGCCT CGCCCGGCA CCCCTCCACG GACGTGGCC CACCCGGAC TGGCAGCCC ACGCACCGT CCTCATCACC GCGCGCACCG GAGCCCTCGG 8400
R R L A R A P L H G R R P T R D W Q P H G T V L I T G G T G A L G

CAGCCACGCC GCACGCTGA TGGCCACCA CCGAGCGAA CACCTCCTCC TGTGAGCG CAGCGCGAA CAAGCCCCCG GAGCCACCA ACTCACCGCC 8500
S H A A R W M A H H G A E H L L L L V S R S G E Q A P G A T Q L T A

FIG. 31Q

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GAACTCACC CATGGGGGC CCGCGTCACC ATCGCCGCTT GCGAGTCGC CGACCCCCAC GCCATGCGA CCTCTCTGA CGCCATCCC GCCGAGACG 8600
E L T A S G A R V T I A A C D V A D P H A M R T L L D A I P A E T P

CCCTCACC GCCTGTCAC ACCGCGGCG CGCTCGACG GGCATCGTG GACACGCTGA CCGCGGAGCA GGTCCGGCGG GCCACCGTG CGAAGGCCGT 8700
L T A V V H T A G A L D D G I V D T L T A E Q V R R A H R A K A V

MluI
▼

CGGCGCCTCG GTGCTCGAC AGCTGACCG GACCTCGAC CTCGACCGT TCGTCTCTT CTCGTCTGTG TCGAGCACTC TGGCATCCC CGGTCAGGCG 8800
G A S V L D E L T R D L D L D A F V L F S S V S S T L G I P G Q G

AACTACGCC CGACAAACG CTACCTCGAC GCCCTGCGG CTGCGCGCGG GGCCACCGG CCGTCCGCGG TCTCGGTGGC CTGGGGACCG TGGACCGTG 8900
N Y A P H N A Y L D A L A A R R R A T G R S A V S V A W G P W D G G

GCGGCATGGC CGCCGCTGAC GCGGTGGCG AGCGGCTGCG CAACACCGG GTGCCCGGCA TGGACCCGGA ACTCGCCCTG GCCGCACTGG AGTCCCGCT 9000
G M A A G D G V A E R L R N H G V P G M D P E L A L A A L E S A L

FIG. 31R

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CGGCCGGGAC GAGACCGCGA TCACCGTCGC GGACATCGAC TGGGACCGCT TCTACCTCGC GTACTCCTCC GGTGCGCCGC AGCCCCCTCGT CGAGGAGCTG 9100
G R D E T A I T V A D I D W D R F Y L A Y S S G R P Q P L V E E L

BstXI



CCCGAGGTGC GCGCGATCAT CGACGCACGG GACAGCGCCA CGTCCGGACA GGGCGGGAGC TCCGCCCAGG GCGCCAACCC CCTGGCCGAG CGGCTGGCCG 9200
P E V R R I I D A R D S A T S G Q G G S S A Q G A N P L A E R L A A

CCGCGGCTCC CCGCGAGCGT ACGGAGATCC TCCTCGGTCT CGTACGGGCG CAGGCGCGCG CCGTGCTCCG GATGCTTCG CCGGAGGACG TCGCGCCCGA 9300
A A P G E R T E I L L G L V R A Q A A A V L R M R S P E D V A A D

CCGCGCCTTC AAGGACATCG GCTTCGACTC GCTCGCCGGT GTCGAGCTGC GCAACAGGCT GACCCGGCG ACCGGGCTCC AGCTGCCCGC GACGCTCGTC 9400
R A F K D I G F D S L A G V E L R N R L T R A T G L Q L P A T L V

TTGACCAACC CGACGCCGCT GGCCTCTGTG TCGCTGCTCC GCAGCGAGTT CCTCGGTGAC GAGGAGACGG CCGACGCCCG GCGGTCCGCG GCGCTGCCCG 9500
F D H P T P L A L V S L L R S E F L G D E E T A D A R R S A A L P A

FIG. 31S

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plkPKS Sequence

10 20 30 40 50 60 70 80 90 100
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

BsaBI

CGACTGTGCG TGCCGGTGCC GCGGCCGGCG CCGGCACCGA TGCCGACGAC GATCCGATCG CGATCGTCCG GATGAGCTGC CGTACCCCG GTGACATCCG 9600
T V G A G A G A G A G T D A D D A D D D P I A I V A M S C R Y P G D I R

CAGCCCGGAG GACTGTGGC GGATGCTGTC CGAGGGCGGC GAGGGCATCA CGCGTTCCC CACCGACCGC GGCTGGGACC TCGACGGCCT GTACGACGCC 9700
S P E D L W R M L S E G G E G I T P F P T D R G W D L D G L Y D A

GACCCGGACG CGCTCGGCAG GCGGTACGTC CCGAGGGCG GGTTCCTGCA CGACGCGGCC GAGTTCGACG CGGAGTTCTT CGGCGTCTCG CCGCGCGAGG 9800
D P D A L G R A Y V R E G G F L H D A A E F D A E F F G V S P R E A

MscI
Bali

CGCTGGCCAT GGACCCGACG CAGCGGATGC TCCTGACGAC GTCTGGGAG GCCTTCGAGC GGGCCGGCAT CGAGCCGGCA TCGCTGCGCG GCAGCAGCAC 9900
L A M D P Q Q R M L L T T S W E A F E R A G I E P A S L R G S S T

CGGTGTCTTC ATCGGCTCTT CCTACCAGGA CTACGCGGCC CCGTCCCGA ACGCCCCCG TGGCGTGAG GGTACCTGC TGACCGGCG CACGCCGAGC 10000
G V F I G L S Y Q D Y A A R V P N A P R G V E G Y L L T G S T P S

FIG. 31T

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plkPKS Sequence

10 20 30 40 50 60 70 80 90 100
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890

GTCGCGTCGG GCCGTATCGC GTACACCTTC GGTCTCGAAG GGCCCGCGAC GACCGTCGAC ACCGCTGCT CGTCGTCGCT GACCGCCCTG CACCTGGCGG 10100
V A S G R I A Y T F G L E G P A T T V D T A C S S S L T A L H L A V

▼
ApaLI

TGCGGGCGGT GCGCAGCGGC GAGTGCACGA TGGCGCTCGC CGGTGGCGTG GCGATGATGG CGACCCCGCA CATGTTCTGT GAGTTCAGCC GTCAGCGGCG 10200
R A L R S G E C T M A L A G G V A M M A T P H M F V E F S R Q R A

GCTCGCCCCG GACGSCGCA GCAAGGCCTT CTCGGCGGAC GCCGACGGT TCGGCGCGC GGAGGCGTC GGCCTGCTGC TCGTGGAGCG GCTCTCGGAC 10300
L A P D G R S K A F S A D A D G F G A A E G V G L L L V E R L S D

▼
KpnI

▼
Acc65I

GCGCGGCGCA ACGGTACCC GGTGCTCGC GTGTCCGCG GTACCGCGT CAACCAGGAC GCGCGCAGCA ACGGGCTGAC CGCGCCCAAC GGACCCCTCGC 10400
A R R N G H P V L A V V R G T A V N Q D G A S N G L T A P N G P S Q

AGCAGCGGGT GATCCGGCAG GCGCTCGCG ACGCCGGCT GGCACCCGGC GACATCGACG CCGTCGAGAC GCACGGCAG GGAACCTCGC TGGGCGACCC 10500
Q R V I R Q A L A D A R L A P G D I D A V E T H G T G T S L G D P

FIG. 31U

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plkPKS Sequence

	20	30	40	50	60	70	80	90	100
1	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
2	CAGGGCCTCC	AGGCCACGTA	CGGCAAGGAG	CGGCCCGCGG	AACGGCCGCT	CGCCATCGGC	TCCGTGAAGT	CCAACATCGG	ACACACCCAG
3	Q G L Q	A T Y G	K E R P	A E R P	L A I G	S V K S	N I G	H T Q	
4	GTGCGGCGG	CATCATCAAG	ATGGTCCTCG	CGATGCGCCA	CGGCACCCCTG	CCGAAGACCC	TCCACGCCGA	CGAGCCGAGC	CCGCACGTCG
5	A A G I	I K M V	L A M R	H G T L	P K T L	H A D	E P S	P H V D	
6	CAGCGGCCTG	GCCCTCGTCA	CCGAGCCGAT	CGACTGGCCG	GCCGGCACCG	GTCCGGCGCG	CGCCGCCGTC	TCCTCCTTCG	GCATCAGCGG
7	S G L A	L V T E	P I D W	P A G T	G P R R	A A V	S S F G	I S G	
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99									
100									

Bsu36I



FIG. 31V

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pkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CCGACGTGGC CCTGCCGGCC GAGGTGCGCG GTGCCGAGGG CGCGCGGTTC GGCCTTCACC CGCGCTGCT CGACGCCGCC GTGCAGGCGG CCGGTGCGGG 23600
 D V A L P A E V A G A E G A R F G L H P A L L D A A V Q A A G A G

CGGGGGCGTT CGGCGGGGC ACGGGCTGC CGTTCGCCTG GAGCGGATC TCCTGTACG GGTGGGCGC ACCGCCCTCC GCGTGGGT GGCCCCCGCC 23700
 R G V R R G H A A A V R L E R D L L Y A V G A T A L R V R L A P A

GGCCCCGACA CGGTGTCCGT GAGCGCGCC GACTCCTCG GGCAGCGGT GTTCGCCGG GACTCCCTCA CGGTGTGTC CGTCGACCCC GCGCAGCTGG 23800
 G P D T V S V S A A D S S G Q P V F A A D S L T V L P V D P A Q L A

CGGCCTTCAG CGACCCGACT CTGGACGCGC TGCACCTGCT GGAGTGAC CCCTGGAC GTGCCGCGCA GGCCCTGCC GCGCGGTG TGCTGGGCGG 23900
 A F S D P T L D A L H L L E W T A W D G A A Q A L P G A V V L G G

CGACGCCGAC GGTCTCGCG CGCGGTGGC ACCAGGTCC TGCTCTCC TGACCTTACG GACCTGTGG AGCCGTCGA CCGGGCGGAG 24000
 D A D G L A A A L R A G G T E V L S F P D L T D L V E A V D R G E

FIG. 31W

plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

SphI
▼

GGCTCTTCC GGCTCGTCA GAGCTGGGC ATCGGCGCG CGCACTGCT CGGTCACTCG GTGGGCGAGA TCGCGCGCG GCACGTGCGG GGTGTGTCT 11600
 A L F R L V E S W G M R P A A L L G H S V G E I A A A H V A G V F S

CGCTGCGCGA CGCGGCGCG CTGCTGCGCG CGCGGCGCG GCTCATGCA GAGTCTCCCG CCGGTGGCGC GATGCTGCGC GTCCAGGCGC CGGAGGACGA 11700
 L A D A A R L V A A R G R L M Q E L P A G G A M L A V Q A A E D E

GATCCGCGTG TGGCTGAGA CGGAGGAGCG GTACGCGGGA CGTCTGGAC TCGCCGCCGT CAACGGCCCC GAGGCGCGC TCCTGTCCCG CGACCGGAC 11800
 I R V W L E T E E R Y A G R L D V A A V N G P E A A V L S G D A D

SphI
▼

GCGGCGCGG AGGCGGAGC GTACTGGTCC GGGCTCGCC GCAGGACCG CGGCTGCGG GTACGCCAG CCTTCCACTC CGGCACATG GACGGCATGC 11900
 A A R E A E A Y W S G L G R R T R A L R V S H A F H S A H M D G M L

TGACGGGTT CGCGGCCCTC CTGAGACCG TGGAGTTCCG GCGCCCTCC CTGACGTGG TCTCGAACCT CACCGGCGCTG GCGCGCGCG CGGAGCACCT 12000
 D G F R A V L E T V E F R R P S L T V V S N V T G L A A G P D D L

FIG. 31X

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

ScaI
▼

GTGCGACCCC GAGTACTGGG TCCGGCAGGT CCGCGGACCC GTCGGCTTCC TCGACGGCGT CCGTGTCCTG CCGGACCTCG GCGTGGGAC CTGCTGGAG 12100
 C D P E Y W V R H V R G T V R F L D G V R V L R D L G V R T C L E

CTGGGCCCCG ACGGGTCTT CACCGCCATG GCGGCGGACG GCCTGCGGGA CACCCCGCGG GATTCGGCTG CCGGCTCCCC CGTGGCTCT CCGCCCGGCT 12200
 L G P D G V L T A M A A D G L A D T P A D S A A G S P V G S P A G S

CTCCCGCCGA CTCGGCCGCC GCGCGGCTCC GGCCCGGCCC GCTGCTCTG GCGCTGCTG CCGGCAAGCG GTGGAGACCG GAGACCGTCG CGGACGCCCT 12300
 P A D S A A G A L R P R P L L V A L L R R K R S E T E T V A D A L

CGGCAGGGCG CAGCCCCACG GCACCGGACC CGACTGGCAC GCCTGGTTCG CCGGCTCCGG GCGGCACCGC GTGGACCTGC CCACGTACTC CTTCCGGCGC 12400
 G R A H A H G T G P D W H A W F A G S G A H R V D L P T Y S F R R

GACCGTACT GGCTGGACGC CCGGGCGGCC GACACCGCGG TGGACACCGC CGGCCTCGGT CTCGGCACCG CCGACACCCC GCTGCTCGGC GCGTGGTCA 12500
 D R Y W L D A P A A D T A V D T A G L G L G T A D H P L L G A V V S

FIG. 31Y

pikPKS Sequence

[illegible]

GCCTTCCGGA CCGGACGGC CTGCTGCTCA CCGGCCGCT CTCCTGCGC ACCACCGT GGCTCGCGA CCAAGCCGTC CTGGGAGCG TCCTGCTCCC 12600

CGGCGCGCG ATGTCGAAC TCGCCGCGCA CGCTCGGAG TCCGCCGGT CCGGTACGT GCGGAGCTG ACCTCCTTG AACGGTGGT ACTGCCGAG 12700
G A A M V E L A A H A A E S A G L R D V R E L T L L E P L V L P E

CACGGTGGG TCGAGCTGG CGTGACGGT GGGCGCCGG CCGAGAGCC CGGTGCGAG TCGGCCGGG ACGGCGACG GCCGTCTCC CTCACATCGC 12800
H G G V E L R V T V G A P A G E P G G E S A G D G A R P V S L H S R

Acc65I KpnI MscI
 Bali

GGCTGGCGA CGGCGCGCC GGTACCGCT GGTCTGCCA CGGACCGGT CTGCTGGCCA CCGACCGCC CGAGTTCCT GTGCGCGCC ACCGTGGGC 12900
L A D A P A G T A W S C H A T G L L A T D R P E L P V A P D R A A

CATGTGGCG CCGCAGGGCG CCGAGGAGT GCGCTCGAC GGTCTTACG AGGGCTCGA CGGAACGGC CTCGCTTCG GTCCGTGTT CCAGGGGTG 13000
 M W P P Q G A E E V P L D G L Y E R L D G N G L A F G P L F Q G L

FIG. 31Z

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

AACGCGGTGT GCGGTACGA GGTGAGTTC TTGCGCTCC CGCCACCACG AATGCGACG CGCCCGCGAC CGGAACGGC GCGGGAGTG 13100
N A V W R Y E G E V F A D I A L P A T T N A T A P A T A N G G G S A

BsmI
▼

CGGCGGCGGC CCCCTACGGC ATCCACCCCG CCTGCTCGA CGTTGCTG CACGCCATCG CGGTGCGCG TCTGTCGAC GAGCCCGAGC TCGTCGCGT 13200
A A A P Y G I H P A L L D A S L H A I A V G G L V D E P E L V R V

ApalI
▼

CCCCTTCAC TGGAGCGTG TCACCGTGCA CGCGGCGCGT GCCGCGTCC TCTGCGCTCC GCGGGGACG ACGCCGTCTC GCTGTCCCTG 13300
P F H W S G V T V H A A G A A A R V R L A S A G T D A V S L S L

ACGGACGGCG AGGACGCCC GCTGGTCTCC GTGGAACGGC TCACGCTGCG CCCGGTCACC GCCGATCAG CGGCGGCGAG CCGGTCGGC GGGCTGATG 13400
T D G E G R P L V S V E R L T L R P V T A D Q A A A S R V G G L M H

ACCGGTGGC CTGGGTCGG TACGCCCTCG CCTGTCGG CGAACAGGAC CGCACGCCA CTTGCTACG GCCGACCGCC GTCTCGGCA AGGACGAGCT 13500
R V A W R P Y A L A S S G E Q D P H A T S Y G P T A V L G K D E L

FIG. 31AA

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GAAGTCGCC GCGGCCCTGG AGTCCGCGGG CGTCGAAGTC GGGCTCTACC CCGACTTGGC CCGGCTGTCC CAGGACGTGG CCGCCGCGGC CCGGGCGCCC 13600
 K V A A A L E S A G V E V G L Y P D L A A L S Q D V A A G A P A P

CGTACCGTCC TTGGCCCGCT GCCCGCGGGT CCGCGCGCAG GCGTGTACGG GGCACGCTGG CCGGACGCT GAGCTGTCTC CAGGCCTGGC 13700
 R T V L A P L P A G P A D G G A E G V R G T V A R T L E L L Q A W L

TGGCCGACGA GCACCTCGCG GGCACCGGCC TGCTCTGTGGT CACCCGCGGT GCGGTGCGGG ACCCGAGGG GTCCGCGGCC GACGATGGCG GCGAGGACCT 13800
 A D E H L A G T R L L L V T R G A V R D P E G S G A D D G G E D L

NotI

GTCCACCGG GCGGCCCTGG GTCTCTGTACG GACCGCGCAG ACCGAGACCC CCGGCCGCTT CCGCCTTCTC GACCTGGCGG ACGACGCTC GTCGTACCGG 13900
 S H A A A W G L V R T A Q T E N P G R F G L L D L A D D A S S Y R

BstXI

ACCCCTGCCGT CCGTGTCTCTC CGACGCGGGC CTGCGCGCAG AACCGCAGCT CGCCCTGCAC GACGGCACCA TCAGGCTGGC CCGCCTGGCC TCCGTCCGGC 14000
 T L P S V L S D A G L R D E P Q L A L H D G T I R L A R L A S V R P

FIG. 31BB

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CCGAGACCGG CACCGCGCA CCGCGCTCG CCGCGGAGG CACGGTCCTG CTGACCGCG GCACGGCGG CCTGGGCGA CTGGTCGCC GGCACGTGGT 14100
E T G T A A P A L A P E G T V L L T G G T G G L G G L V A R H V V

▼
ApaLI

GGGCGAGTGG GGCCTACGAC GCCTGCTGCT GGTGAGCCG CCGGGCACGG ACGCCCCGG CGCCGACGAG CTCGTGCACG AGCTGGAGGC CCTGGGAGCC 14200
G E W G V R R L L L V S R R G T D A P G A D E L V H E L E A L G A

GACGTCTCGG TGGCCGCGTG CGACGTCGCC GACCGCGAAG CCTCACCGC CGTACTCGAC GCCATCCCCG CCGAACACCC GCTCACCGCG GTCGTCCACA 14300
D V S V A A C D V A D R E A L T A V L D A I P A E H P L T A V V H T

CGGCAGGCGT CCTCTCCGAC GGCACCTCC CGTCCATGAC GACGGAGGAC GTGGAACACG TACTGCGGCC CAAGGTCGAC GCCGCGTTCC TCCTCGACGA 14400
A G V L S D G T L P S M T T E D V E H V L R P K V D A A F L L D E

ACTACCTCG ACGCCCGCAT ACGACCTGGC AGGTTCTGTC ATGTTCTCCT CCGCCCGCCG CGTCTTCGGT GCGCGGGGCG AGGGCGCCTA CGCCGCCGCC 14500
L T S T P A Y D L A A F V M F S S A A A V F G G A G Q G A Y A A A

FIG. 31CC

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

AAGCCACCC TCGACGCCCT CGCCTGGGCG CGCCGGGCGAG CCGGACTCCC CGCCCTCTCC CTCGGCTGGG GCCTCTGGG CGAGACCAGC GGCATGACCG 14600
 N A T L D A L A L A W R R R A A G L P A L S L G W G L W A E T S G M T G

GGGAGCTCGG CCAGGCGGAC CTGCGCCCGA TGAGCCGCGC GGGCATCGGC GGGATCAGCG ACGCCGAGGG CATCGCGCTC CTCGACGCGG CCCTCCGCGA 14700
 E L G Q A D L R R M S R A G I G G I S D A E G I A L L D A A L R D

CGACCGCCAC CCGGTCTGTC TGCCCTGCG GCTCGACGCC GCCGGGCTGC GGGGACGAC CCGGCCGGA TCCCGGCGCT CTTCCGCGAC 14800
 D R H P V L L P L R L D A A G L R D A A G N D P A G I P A L F R D

GTCTGCGGCG CCAGGACCGT CCGGGCCCGG CCGTCCGCGG CCTCCGCTC GACGACAGCC GGGACGCGG GCACGCCGGG GACGCGGAC GGC CGCGCGG 14900
 V V G A R T V R A R P S A A S T T A G T A G T P G T A D G A A E

XhoI
 PaeR7I

AAACGCGGCG GGTACGCTC GCCGACCGG GCCGCGGCC CGCCACCGT GGACGGGCCC GCACGGCAGC GCCTGCTGCT CGAGTTCGTC GTCGCGGAGG TCGCCGAAGT 15000
 T A A V T L A D R A A T V D G P A R Q R L L L E F V V G E V A E V

FIG. 31DD

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pkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

Seal

▼
 ACTCGGCCAC GCCCGCGGTC ACGGATCGA CGCCGAACGG GGTTCCTCG ACCTCGGCTT CGACTCCCTG ACGCGCTCG AACTCCGCAA CCGGCTCAAC 15100
 L G H A R G H R I D A E R G F L D L G F D S L T A V E L R N R L N

TCCGCGGCTG GCCTGCGCCT CCCGGGACC CTGGTCTTCG ACCACCCAAG CCCGGGCGCA CTCGCTCC ACCTGGACGC CGAGCTGCCG CGCGGCGCCT 15200
 S A G G L A L P A T L V F D H P S P A A L A S H L D A E L P R G A S

CGGACCAGGA CGGAGCCGGG AACCGGAAC GGAACGAGAA CGGACGACG GCGTCCCGA GCACCGCGG CAGCGACCG CTGCTGGCAC AACTGACCCG 15300
 D Q D G A G N R N G N E N G T T A S R S T A E T D A L L A Q L T R

CCTGGAGGC GCCTTGGTGC TGACGGCCT CTGGACGCC CCCGGAGCG AAGAAGTCTT GGAGCACCTG CCGTCCCTGC GCTCGATGGT CACGGCGGAG 15400
 L E G A L V L T G L S D A P G S E E V L E H L R S L R S M V T G E

ACCGGACCG GGACCGGCTC CGGAGCCCCG GGTCCGGCCG GACGCGGCCG CGAGGACCG CCCTGGGCGG CCGGGGACCG AGCCGGGGGC GGGAGTGAGG 15500
 T G T G T A S G A P D G A G S G A E D R P W A A G D G A G G G S E D

FIG. 31EE

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

BspHI

▼
ACGGCGCGG AGTGCGGAC TTCATGAAC CCTCGGCGG GGAATCTTC GGCTCTCTG ACCAGGACCC CAGCACGGAC TGATCCCTGC CGCAGCGTCG 15600
G A G V P D F M N A S A E E L F G L L D Q D P S T D

XmnI

▼
CCTCCCGCC CGGACCCCGT CCGGGCACC TCGACTCGAA TCACTTCATG CGCGCTCGG GCGCTCCAG GAACTCAGG GGAAGCGTG TCCACGGTGA 15700
V S T V N

ACGAAGAGAA GTACCTCGAC TACCTGCGTC GTGCCACGGC GGACTCCAC GAGGCCCGTG GCCGCCTCCG CGAGCTGGAG GCGAAGGCGG GCGAGCCCGT 15800
E E K Y L D Y L R R A T A D L H E A R G R L R E L E A K A G E P V

GGCGATCGTC GGCATGGCCT GCGGCTGCG CCGCGGCGTC GCCTCGCCCG AGGACCTGTG GCGGCTGGTG GCCGCGCGG AGGACGCGAT CTCGGAGTTC 15900
A I V G M A C R L P G G V A S P E D L W R L V A G G E D A I S E F

CCCCAGGACC GCGGCTGGGA CGTGGAGGGC CTGTACGACC CGAACCGGA GGCCACGGG AAGAGTTACG CCCGCGAGGC CGGATTCCTG TACGAGGCGG 16000
P Q D R G W D V E G L Y D P N P E A T G K S Y A R E A G F L Y E A G

FIG. 31FF

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GCGAGTTTGA	CGCCGACTTC	TTGGGATCT	CGCCGCGGGA	GGCCCTCGCC	ATGGACCCGC	AGCAGGTCT	CCTCCTGGAG	GCTCCTGGG	AGCGTTTGA
E F D	A D F	F G I S	P R E A L A	M D P Q	Q R L L L E	A S W E	A F E		
BamHI									
▼									
GCAAGCGGG	ATCCCGGGG	CCACCGGCG	CGGCACCTCG	GTGCGGTCT	TCACCGCGCT	GATGTACCAC	GACTACGCCA	CCCGTCTCAC	CGATGTCCCG
H A G	I P A A	T A R G	T S V G V F	T G V M Y H	D Y A T	R L T D	V P		
GAGGCAATCG	AGGGTACCT	GGGCACGGC	AACTCCGGCA	GTGTGCGCTC	GGGCGCGTC	GCGTACACGC	TTGGCCTGGA	GGGCGCGCC	GTCACGGTCG
E G I E	G Y L G	T G N S G S	V A S G R V	A Y T L G L E	G P A V	T V D			
ACACCGCCTG	CTCGTCCTCG	CTGGTGCCC	TGCACCTCGC	CGTGCAGGCC	CTGCCAAGG	GCGAGGTGGA	CATGGCGCTC	GCCGCGGCG	TGACGGTCAT
T A C	S S S L	V A L H L A	V Q A L R K G	E V D M A L	A G G V	T V M			
XmnI									
▼									
GTGACGCCC	AGCACCTTCG	TCGAGTTTCAG	CCGTACGCG	GGCTGGGCG	CGGACGGCG	GTGGAAGTCC	TTCTCGTTCGA	CGGCCGACCG	CACCAGCTGG
S T P	S T F V	E F S R Q R	G L A P D G R	S K S F S S	T A D G	T S W			

FIG. 31GG

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

BamHI
▼

TCCGAGGGCG TCGGCGTCCT CCTCGTCGAG CGCCTGTCCG ACGGCGGTG CAAGGGCCAT CGGATCCTCG CCGTGTGTCG GGGCACCGCC GTCAACACG 16600
 S E G V G V L L V E R L S D A R R K G H R I L A V V R G T A V N Q D

ACGGGCGCAG CAGGCGCCTC ACGGCTCGA ACGGCGCGTC GCAGCAGCGC GTCATCCGAC GTGCCCTGGC GGACGCCCGG CTCACGACCT CCGACGTGGA 16700
 G A S S G L T A P N G P S Q Q R V I R R A L A D A R L T T S D V D

CGTCGTGCGAG GCCACAGGCA CGGTACGG ACTCGGCGAC CCGATCGAGG CGCAGGCGGT CATCGCCACG TACGGGCGG GCCGTGACGG CGAACAGCGG 16800
 V V E A H G T G T R L G D P I E A Q A V I A T Y G Q G R D G E Q P

BclI
▼

CTGCGCCTCG GGTGTTGAA GTCCAACATC GGACACACCC AGGCGCGCGC CGGTGTCTCC GCGGTGATCA AGATGGTCCA GCGCATGCGC CACGGCGTCC 16900
 L R L G S L K S N I G H T Q A A A G V S G V I K M V Q A M R H G V L

PmlI
▼

TGCCGAGAC GCTCCACGTG GAGAAGCGA CCGACCAGGT GGACTGGTCC GCGGCGCGG TCGAGCTGCT CACCGAGGCC ATGACTGGC CGGACAGGG 17000
 P K T L H V E K P T D Q V D W S A G A V E L L T E A M D W P D K G

FIG. 31HH

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CGACGGCGGA CTGCGCAGGG CCGCGGTCTC CTCCTTCGGC GTACAGCGGA CGAACGCGCA CGTCGTGCTC GAAGAGGCC CCGCGGCCGA GGAGACCCCT 17100
 D G G L R R A A V S S F G V S G T N A H V V L E E A P A A E E T P

GCCTCCGAGG CGACCCCGGC CGTCGAGCCG TCGGTCCGGC CCGGCTGGT GCCGTGGCTG GTGTCCGCGA AGACTCCGGC CGCGCTGGAC GCCAGATCG 17200
 A S E A T P A V E P S V G A G L V P W L V S A K T P A A L D A Q I G

AscI
 ▼

GACGCTCGC CCGGTTGCC TCGCAGGCG GTACGGACGC CGCGCATCCG GCGCGGTGCTG CTCGCGTACT GGCGCGCGGG CGCGCCGAGT TCGAGCACCG 17300
 R L A A F A S Q G R T D A A D P G A V A R V L A G G R A E F E H R

GGCGTCGTG CTCGGCACCG GACAGGACGA TTTCCGCGCAG GCGCTGACCG CTCGGAAGG ACTGATACGC GGCACGCCCT CGGACGTGG CCGGTTGGCG 17400
 A V V L G T G Q D D F A Q A L T A P E G L I R G T P S D V G R V A

XmnI
 ▼

TTGCTGTTCC CCGGTCAGGG CACGCAGTGG GCCGGGATGG GCGCCGAACT CCTCGACGTG TCGAAGGAGT TCGCGCGCGC CATGGCCGAG TCGGAGAGCG 17500
 F V F P G Q G T Q W A G M G A E L L D V S K E F A A M A E C E S A

FIG. 31II

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plPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

ASCI
▼

CGCTCTCCCG CTATGTCGAC TGGTCGCTGG AGCCGTCGT CCGGCAGGCG CCGGGCGCGC CCACGCTGGA GCGGTCGAC GTCGTCCAGC CCGTGACCTT 17600
L S R Y V D W S L E A V V R Q A P G A P T L E R V D V V Q P V T F

CGCTGTCATG GTTTCGCTGG CGAAGTCTG GCAGCACCAC GGGGTGACGC CGCAGGCCGT CGTCGGCCAC TCGCAGGCG AGATCGCCGC CCGGTACGTC 17700
A V M V S L A K V W Q H H G V T P Q A V V G H S Q G E I A A A Y V

GCGGTGCC TCACCTCGA CGAGCGCGC CCGTCTGTC CAATCCATC GCCGCCACC TCGCCGGCAA GGGCGGCATG ATCTCCCTCG 17800
A G A L T L D D A A R V V T L R S K S I A A H L A G K G G M I S L A

CCCTCAGCGA GGAAGCCACC CCGCAGCGCA TCGAGAACCT CCACGACTG TCGATCGCCG CCGTCAACGG CCCACCGCC ACCGTGGTTT CCGGCGACCC 17900
L S E E A T R Q R I E N L H G L S I A A V N G P T A T V V S G D P

CACCCAGATC CAAGAGCTCG CTCAGGCGTG TGAGGCCGAC GGGGTCCGCG CACGGATCAT CCCCCTCGAC TAGCCTCCC ACAGCGCCA CCGTCGAGACC 18000
T Q I Q E L A Q A C E A D G V R A R I I P V D Y A S H S A H V E T

FIG. 31JJ

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

EspI
Bpu1102I
Bsu36I

ATCGAGAGCG AACTCGCCGA GGTCTCTGCC GGGCTCAGCC CGCGACACCC TGAGTGCCG TTCTTCTCGA CACTCGAAGG CGCTGGATC ACCGAGCCG 18100
I E S E L A E V L A G L S P R T P E V P F F S T L E G A W I T E P V

KpnI
Acc65I

TGCTCGACGG CACTTACTGG TACCGCAACC TCCGCCACCG CGTCGGCTTC GCCCGGCCG TCGAGACCCCT CGCCACCGAC GAAGCTTCA CCCACTTCAT 18200
L D G T Y W Y R N L R H R V G F A P A V E T L A T D E G F T H F I

CGAGGTGAGC GCCACCCCG TCCTCACCAT GACCTTCCCG GAGACCGTCA CCGGCTCCG CACCTCCCG CGCGAACAGG GAGGCCAGGA GCGTCTGGTC 18300
E V S A H P V L T M T L P E T V T G L G T L R R E Q G G Q E R L V

ACCTCACTCG CGAAGCCTG GACCAACGGC CTCACCATCG ACTGGGCGCC CGTCCTCCCG ACCGCAACCG GCCACACCC CGAGCTCCCC ACCTACGCT 18400
T S L A E A W T N G L T I D W A P V L P T A T G H H P E L P T Y A F

TCCAGCGCGG TCACTACTGG CTCCACGACT CCCCAGCGCT CCAGGGCTCC GTGCAGGACT CCTGGCGCTA CCGCATCGAC TGAAGCGCC TCGCGGTCCG 18500
Q R R H Y W L H D S P A V Q G S V Q D S W R Y R I D W K R L A V A

FIG. 31KK

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pikPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

MluI



CGACGGCTCC GAGCGCGCCG GGCTGTCCGG GCGCTGGCTC GTCGTGCTCC CCGAGGACCG TTCCGCCGAG GCCGCCCGG TGTGCGCCG GCTGTCCGCG 18600
 D A S E R A G L S G R W L V V V P E D R S A E A A P V L A A L S G

GCCGGCGCCG ACCCGGTACA GCTGGACGTG TCCCGCTGG GCGACCGGCA GCGGCTCGCC GCGACGCTGG GCGAGGCCCT GCGGCGGCC GGTGGAGCCG 18700
 A G A D P V Q L D V S P L G D R Q R L A A T L G E A L A A A G G A V

TCGACGGCGT CCTCTCGCTG CTCGCGTGGG ACGAGAGCGC GCACCGCGGC CACCCCGCC CCTTCACCG GGGCACCGGC GCACCCCTCA CCCTGTRGCA 18800
 D G V L S L L A W D E S A H P G H P A P F T R G T G A T L T L V Q

GGCGCTGGAG GACGCGCGCG TCGCCGCCCC GCTGTGCTGC GTGACCCACG GCGCGGTGTC CGTCGGCCCG GCGACCAAG TCACCTCCCC CGCCCGGCC 18900
 A L E D A G V A A P L W C V T H G A V S V G R A D H V T S P A Q A

ATGCTGTGGG GCATGGGCGG GGTGCGCGCC CTGGAGCACC CCGAGCGGTG GGGCGGCTG ATCGACCTGC CCTCGGACGC CGACCGGGCG GCCCTGGACC 19000
 M V W G M G R V A A L E H P E R W G G L I D L P S D A D R A A L D R

FIG. 31LL

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GCATGACCAC GGTCTCTGCC GGGCGTACGG GTGAGGACCA GGTGCGGTA CGCGCTCCG GGCTGCTCG CGCGGCCTC GTCCGGCCT CCCTCCCGC 19100
 M T T V L A G G T G E D Q V A V R A S G L L A R R L V R A S L P A

NotI



GCACGGCAG GCTTCGCCGT GGTGGCAGGC CGACGGCAG GTGCTCGTCA CCGTGCCGA GGAGCCTGCG GCCGCCGAG CCGCAGCAG GCTGGCCCGC 19200
 H G T A S P W Q A D G T V L V T G A E E P A A A E A A R R L A R

GACGGCGCG GACACCTCCT CCTCCACACC ACCCCTCCG GCAGCGAAG CGCCGAGGC ACCTCCGCTG CCGCCGAGGA CTCGGGCCTC GCCGGGCTCG 19300
 D G A G H L L L H T T P S G S E G A E G T S G A A E D S G L A G L V

NotI



TCGCCGAAC CGCGGACCTG GGGCGGACGG CCACCGTCGT GACCTGGGAC CTCACGGACG CGGAGGCGGC CGCCCGGCTG CTCGGCCGCG TCTCCGACGC 19400
 A E L A D L G A T A T V V T C D L T D A E A A A R L L A G V S D A

EspI

Bpu1102I



GCACCCGCTC AGCGCGCTCC TCCACCTGCC GCCACCGTC GACTCCGAGC CGCTCGCCGC GACCGACGCG GACCGGCTCG CCCGTGTGCT GACCGCGAAG 19500
 H P L S A V L H L P P T V D S E P L A A T D A D A L A R V V T A K

FIG. 31MM

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pikPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GCACCGCCG CGCTCCACCT GGACCGCCTC CTGCGGAGG CCGCGGCTGC CGAGGCCGT CGGCCCGTCC TGGTCCTCTT CTCCTCGGTC GCCGCGATCT 19600
 A T A A L H L D R L L R E A A A A G G R P P V L V L F S S V A A I W

GGGGCGGGC CGGTACGGC GCGTACGGC CTTCTCGAC GCCCTGCGG GTCAGCACCG GGCCGACGGC CCCACCGTGA CCTCGGTGGC 19700
 G G A G Q G A Y A A G T A F L D A L A G Q H R A D G P T V T S V A

CTGGAGCCCC TGGAGGGCA GCCGCGTCAC CGAGGGTGG ACCGGGAGC GGCTGCGCG CTTGGGCTG CGCCCCCTCG CCCCCCGGAC GCGGCTCACC 19800
 W S P W E G S R V T E G A T G E R L R R L G L R P L A P A T A L T

GCCCTGGACA CCGCGCTCG CCACGGCGAC ACCGCGGTCA CGATCGCGCA CGTCGACTGG TCGAGCTTCG CCCCCGGCTT CACCACGGCC CGGCCGGGCA 19900
 A L D T A L G H G D T A V T I A D V D W S S F A P G F T T A R P G T

Asci



CCCTCCTCGC CGATCTGCCC GAGGCGGCC CCGCGCTCGA CGAGCAGCAG TCGACGACG CCGCGGACGA CACCGTCTG AGCCGCGAGC TCGGTGCGCT 20000
 L L A D L P E A R R A L D E Q Q S T T A A D D T V L S R E L G A L

FIG. 31NN

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CACCGGCGCC GAACAGCAGC GCCGTATGCA GGAGTTGGTC CGCGAGCACC TCGCCGTGGT CCTCAACCAC CCCTCCCCCG AGCCCGTCGA CACGGGGCGG 20100
 T G A E Q Q R R M Q E L V R E H L A V V L N H P S P E A V D T G R

BstXI
 ▼

GCCTTCGGTG ACCTCGGATT CGACTCGCTG ACGGCGGTG AGCTCCGCAA CCGCCTCAAG AACGCCACCG GCCTGGCCCT CCGGCCACT CTGGTCTTCG 20200
 A F R D L G F D S L T A V E L R N R L K N A T G L A L P A T L V F D

ACTACCCGAC CCCCCGAGC CTGGCGGAGT TCCTCCTCGC GGAGATCCTG GCGAGCAGG CCGGTGCCG CGAGCAGCTT CCGGTGGACG GCGGGGTGCG 20300
 Y P T P R T L A E F L L A E I L G E Q A G A G E Q L P V D G G V D

CGACGAGCCC GTCGCGATCG TCGGCATGGC GTGCCGCTG CCGGGCGGTG TGCCTCGCC GGAGGACTG TGGCGGCTGG TGGCCGCGCG CGAGGACGCG 20400
 D E P V A I V G M A C R L P G G V A S P E D L W R L V A G G E D A

MluI
 ▼

ATCTCCGGCT TCCCGCAGGA CCGCGGCTGG GACGTGGAGG GGCTGTACGA CCGGACCCG GACGCGTCCG GCGGACGTA CTGCCGTGCC GGTGGCTTCC 20500
 I S G F P Q D R G W D V E G L Y D P D P D A S G R T Y C R A G G F L

FIG. 3100

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pkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

TCGACGAGGC GGGCGAGTTC GACGCCGACT TCTTCGGGAT CTGCGCGCGC GAGGCCCTCG CCATGGACCC GCAGCAGCGG CTCCTCCTTG AGACCTCCTG 20600
D E A G E F D A D F F G I S P R E A L A M D P Q Q R L L L E T S W

GGAGGCGGTC GAGGACGCCG GGATCGACCC GACCTCCCTT CAGGGGCAGC AGGTCGGCGT GTTCGCGGCG ACCAACGGCC CCCACTACGA CCCGCTGCTC 20700
E A V E D A G I D P T S L Q G Q Q V G V F A G T N G P H Y E P L L

CGCAACACCG CCGAGGATCT TGAGGGTTAC GTCGGGACCG GCAACGCCG CAGCATCATG TCGGGCCGTG TCTCGTACAC CCTCGGCCTG GAGGCCCGG 20800
R N T A E D L E G Y V G T G N A A S I M S G R V S Y T L G L E G P A

BsmI



CCGTCACGGT CGACACCGCC TGCTCCTCCT CGCTGCTGCG CCTGCACCTC GCCGTGCAGG CCCTGCGCAA GGGCGAATGC GGACTGGCGC TCGCGGCGG 20900
V T V D T A C S S S L V A L H L A V Q A L R K G E C G L A L A G G

XmnI



TGTGACGGTC ATGTCGACGC CCACGACGTT CGTGGAGTTC AGCCGGCAGC GCGGGCTCGC GGAGGACGGC CGGTGGAAGG CGTTGCGCGC GTCGCGGAC 21000
V T V M S T P T T F V E F S R Q R G L A E D G R S K A F A A S A D

FIG. 31PP

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

SphI
▼

GGCTTCGGCC CGGCGGAGGG CGTCGGCATG CTCCTCGTCG AGCGCCTGTC GGACGCCCGC CGCAACGGAC ACCGTGTGCT GCGGTCGTG CGCGGCAGCG 21100
 G F G P A E G V G M L L V E R L S D A R R N G H R V L A V V R G S A

CGGTCAACCA GGACGGCGG AGCAACGGCC TGACCGGCC TCGCAGCAGC GCGTCATCG GCGCGGCTC GCGGACGCC GACTGACGAC 21200
 V N Q D G A S N G L T A P N G P S Q Q R V I R R A L A D A R L T T

CGCGGACGTG GACGTCGTG AGGCCACGG CACGGGCGCG CGACTCGGCG ACCCGATCGA GGCACAGGCC CTCATCGCCA CCTACGGCCA GGGGCGCGAC 21300
 A D V D V V E A H G T G T R L G D P I E A Q A L I A T Y G Q G R D

ACCGAACAGC CGCTGGCCTT GGGGTCGTTG AAGTCCAACA TCGGACACAC CCAGGCGGCC GCCGGTGTCT CCGGCATCAT CAAGATGGTC CAGGCGATGC 21400
 T E Q P L R L G S L K S N I G H T Q A A A G V S G I I K M V Q A M R

PmlI
▼

GCCACGGCGT CCTGCCGAG ACGTCCACG TGGACCGGCC GTGCGACCAG ATCGACTGGT CGGCGGGCAC GGTGAGCTG CTCACCGAGG CCATGGACTG 21500
 H G V L P K T L H V D R P S D Q I D W S A G T V E L L T E A M D W

FIG. 31QQ

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GCGGAGGAAG	CAGGAGGGCG	GGCTGCGCCG	CGCGGCGGTC	TCCTCCTTCG	GCATCAGCGG	CACGAACGCG	CACATCGTGC	TGGAAGAAGC	CCCGTCGAC
P R K Q E G G L R R A A V S S F G I S G T N A H I V L E E A P V D									
GAGGACGCCC	CGGCGGACGA	GCGGTGCGTC	GCGGCTGTGG	TGCCGTGGCT	CGTGTCCGCG	AAGACTCCGG	CCGCGCTGGA	CGCCAGATC	GGACGCTCG
E D A P A D E P S V G G V V P W L V S A K T P A A L D A Q I G R L A									
CCGCGTTTCG	CTCGCAGGCG	CGTACGGACG	CCGCGGATCC	GGGCGCGGTC	GCTCGCGTAC	TGGCCGCGCG	GCGTGCGCAG	TTCGAGCACC	GGGCGCTCG
A F A S Q G R T D A A D P G A V A R V L A G G R A Q F E H R A V A									
		NotI		Bsu36I					
GCTCGGACCC	GGACAGGACG	ACCTGGCGGC	CGCACTGGCC	GCGCCTGAGG	GTCGTGTCGG	GGGTGTGGCC	TCCGCTGTGG	GTCGAGTGGC	GTTCTGTGTC
L G T G Q D D L A A A L A A P E G L V R G V A S G V G R V A F V F									
								XmnI	
CCGGGACAGG	GCACGCAGTG	GGCCGGGATG	GGTGCCGAAC	TCCTCGACGT	GTCGAAGGAG	TTCGCGGCGG	CCATGGCCGA	GTGCGAGGCC	GCGCTCGCTC
P G Q G T Q W A G M G A E L L D V S K E F A A A M A E C E A A L A P									

FIG. 31RR

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

ASCI
▼

CGTACGTGGA CTGGTCGCTG GAGGCCGTCG TCCGACAGGC CCCCGGCGCG CCCACGCTGG AGCGGCTCGA TGTCGTCCAG CCGGTGACGT TCGCCGTGCAT 22100
Y V D W S L E A V V R Q A P G A P T L E R V D V V Q P V T F A V M

GGTCTCGCTG GCGAAGGTCT GGCAGCACCA CGGGGTGACC CCGCAAGCCG TCGTCGGCCA CTCGACGGGC GAGATCGCCG CCGGTGACGT CGCCGGTGCC 22200
V S L A K V W Q H H G V T P Q A V V G H S Q G E I A A A Y V A G A

EspI
Bpu1102I
▼

SphI
▼

CTGAGCCTGG ACGACGCCGC TCGTGTCTGT ACCCTGGCA GCAAGTCCAT CGGCGCCAC CTCGCGGGCC AGGGCGGCAT GCTGTCCCTC GCGCTGAGCG 22300
L S L D D A A R V V T L R S K S I G A H L A G Q G G M L S L A L S E

AGGCGGCCGT TGTGAGCGA CTGGCCGGGT TCGACGGGCT GTCCGTGCGC GCCGTCAACG GGCCTACGC CACCGTGGTT TCGGGCGACC CGACCCAGAT 22400
A A V V E R L A G F D G L S V A A V N G P T A T V V S G D P T Q I

CCAAGAGCTC GCTCAGGCGT GTGAGGCCGA CGGGGTCCGC GCAAGGATCA TCCCGGTGCA CTACGCCTCC CACAGCGCC ACGTCGAGAC CATCGAGAGC 22500
Q E L A Q A C E A D G V R A R I I P V D Y A S H S A H V E T I E S

FIG. 31SS

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GAAGTCGCGG ACGTCCTGGC GGGGTGTGTC CCCCAGACAC CCCAGGTCCC CTCTCTCTCC ACCCTCGAAG GCGCCTGGAT CACCGAACCC GCCTCGACG 22600
 E L A D V L A G L S P Q T P Q V P Q F F S T L E G A W I T E P A L D G

KpnI
 Acc65I

MscI
 BalI

GGGGTACTG GTACCGCAAC CTCGCCCATC GTGTGGGCTT CGCCCCGGCC GTCGAATCCC TGGCCACCGA CGAAGGCTTC ACCCACTTCG TCGAGGTGAG 22700
 G Y W Y R N L R H R V G F A P A V E T L A T D E G F T H F V E V S

CGCCCCACCC GTCCTCACCA TGGCGGTGCC CGAGACCGTC ACCGGACTCG GCACCTCTCG CCGTGACAAC GCGGACAGC ACCGCCTCAC CACCTCCCTC 22800
 A H P V L T M A L P A L P E T V T G L G T L R R D N G G Q H R L T T S L

GCCGAGGCTT GGGCCAACGG CCTCACCCTC GACTGGGCTT CTCTCCTCCC CACCACGACC ACCCACCCCG ATCTGCCAC CTACGCCTTC CAGACCGAGC 22900
 A E A W A N G L T V D W A S L L P T T T T H P D L P T Y A F Q T E R

Eco47III

GCTACTGGCC GCAGCCGAC CTCTCCGCG CCGGTGACAT CACTCCGCC GGTCTCGGG CGGCCGAGCA CCCGCTGCTC GCGCGGCCG TGGCGCTCGC 23000
 Y W P Q P D L S A A G D I T S A G L G A A E H P L L G A A V A L A

FIG. 31TT

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plPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GGACTCCGAC	GGCTGCCCTGC	TCACGGGGAG	CCTCTCCCTC	CGTACGCACC	CCTGGCTGGC	GGACCACGCG	GTGGCCGGCA	CCGTGCTGCT	GCCGGGAACG
D S D	G C L L	T G S L	S L S L	R T H P	W L A D	H A V A	G T V L	L L P G	T
GGTTTCGTGG	AGCTGGCGTT	CCGAGCCGGG	GACCAGGTGC	GTTGCGATCT	GGTCGAGGAG	CTCACCTCTC	ACGCGCGCT	CGTCTGCCC	CGTCGTGGCG
A F V E	L A F R	A G D Q	V G C D	L V E L	T L D A	P L V L	P R R G	A	
CGGTCCGTGT	GCAGCTGTCC	GTCCGGCGGA	GCGACGAGTC	CGGGCGTCGT	ACCTTCGGGC	TCTACGCGCA	CCCGGAGGAC	GCGCCGGGCG	AGCGGAGTG
V R V Q	L S V G	A S D E	S G R R	T F G L	Y A H P	E D A P	G E A E	W	
GACGCGCAC	GCCACCGGTG	TGCTGGCCGC	CCGTGCGGAC	CGCACCGCCC	CCGTGCGCCA	CCCGGAGGCC	TGGCCGCCGC	CGGGCGCCGA	GCCGTTGGAC
T R H A	T G V L	A A R A	D R A D	R T A P	V A D P	E A W P	P P G A	E P V D	
GTGACGGTC	TGTACGAGCG	CTTCGGCGCG	AACGGCTACG	GCTACGGCCC	CCTCTTCCAG	GGGTCCGTG	GTGTCTGGCG	GCGTGGCGAC	GAGGTGTTCG
V D G L	Y E R F	A A N G	Y G Y G	Y G P L	F Q G V	R G V W	R R R G	D E V F	A

Eco47III

Eco47III

FIG. 31UU

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CCGACGTGGC	CCTGCCGGCC	GAGGTGCGCG	GTGCCGAGGG	CGCGGGTTC	GGCCTTCACC	CGCGCTGCT	CGACGCCGCC	GTGCAGGCGG	CCGCTGCGGG
D V A	L P A	E V A	G A E	G A R	F G L	H P A	L L D	A A V	Q A A
G A G	A	G	A	E	G	A	R	F	G
CGGGGGCGTT	CGGCGCGGC	ACGCGGCTGC	CGTTGCGCTG	GAGCGGGATC	TCCTGTACGC	GGTCGGCGCC	ACCGCCCTCC	CGCTGCGGCT	GGCCCCCGCC
R G V	R R G	H A A	A A V	R L E	R D L	L Y A	V G A	T A L	R V R
L A	A	A	A	A	A	A	A	A	A
GGCCCGGACA	CGGTGTCCGT	GAGCGCGCC	GACTCCCTCCG	GGCAGCCGGT	GTTCCGCCGG	GACTCCCTCA	CGGTGCTGCC	CGTCGACCCC	GGCAGCTGG
G P D	T V S	V S A	A D S	S G Q	P V F	A A D	S L T	V L P	V D P
A A	A	A	A	A	A	A	A	A	A
CGGCCTTCAG	CGACCCGACT	CTGACCGCGC	TGCACCTGCT	GGAGTGGACC	GCCTGGGACG	GTGCCGGCA	GGCCCTGCCC	GGCGGGTGC	TGCTGGGCGG
A F S	D P T	L D A	L H L	L L E	W T A	W D G	A A Q	A L P	G A V
L A	L	A	L	L	L	L	L	L	L
CGACGCGGAC	GGTCTGCGCG	CGGCGGTGCG	CGCGGTGGC	ACGAGGTCC	TGTCCTTCCC	GGACCTTACG	GACCTGCTGG	AGGCCGTGCA	CCGGGGCGGAG
D A D	G L A	A A	L R A	G G	T E V	L S F	P D L	T D L	V E A
A A	A	A	A	A	A	A	A	A	A

FIG. 31W

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
ACCCCGGCC	CGGCGACCGT	CCTGTGGCC	TGCCCCGCC	CCGGCCCGA	TGGCCCGAG	CATGTCGGG	AGGCCCTGCA	CGGTCGCTC	GCGCTGATGC
T P A P	A T V A	L V A	C P A A	G P D	G P E	H V R E	A L H G	S L A	L M Q
AGGCTTGGCT	GGCGGACGAG	CGGTTACCG	ATGGGCGCCT	GGTGCTCGTG	ACCGCGGACG	CGGTGCGCG	CCGTTCCGGC	GACGGCCTGC	GGTCCACGGG
A W L A	D E R F	T D G R	L V L V	T R D A	V A A	R S G	D G L R	S T G	
ACAGGCGGCC	GTCTGGGGCC	TCGGCCGGTC	CGCGGACGACG	GAGAGCCCGG	GCCGGTTCGT	CCTGCTCGAC	CTCGCCGGGG	AAGCCCGGAC	GGCCGGGGAC
Q A A V	W G L G	R S A Q	T E S P	G R F V	L L D	L A G E	A R T A	G D	
GCCACCGCCG	GGGACGGCCT	GACGACCGGG	GACGCCACCG	TCGGCGGCAC	CTCTGGAGAC	GCCGCCCTCG	GCGACCGCC	CTCGGCTCGG	24400
A T A G	D G L T	T G D A	T V G G	T S G D	A A L G	S A L A	T A L G	S G	
GCGAGCCGCA	GCTCGCCTC	CGGACGGGG	CGCTCCTCGT	ACCCCGCCTG	GCGGGGCGG	CCGCGCCCGC	CGCGGCGGAC	GGCCTCGCCG	CGGCCGACGG
E P Q L	A L R D	G A L L	V P R L	A R A A	A P A	A A D	G L A A	A D G	24500

FIG. 31WW

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CCTCGCCGCT	CTGCGGCTGC	CCGCCGCTCC	GGCCCTCTGG	CGTCTGGAGC	CCGTACGGA	CGGCAGCCTG	GAGAGCCTCA	CGGCGGCGCC	CGGCGACGCC
L A A	L P L P A A P	A A P A L W	R L E P G T D	G S L E S L T	A A P G D A				
24600									
GAGACCTCG	CCCCGGAGCC	GCTCGGCCCG	GGACAGGTCC	GCATCCGAT	CCGGGCCACC	GGTCTCAACT	TCCGCGACGT	CCTGATCGCC	CTCGGCATGT
E T L A	P E P L G P G Q V R	I A I R A T	G L N F R D V	L I A L G M Y					
24700									
ACCCGATCC	GGGCTGATG	GGCACCAGG	GAGCGGCGT	GGTCACCGG	ACCGGCCCG	GGTCACGCA	CCTCGCCCC	GGCGACCGG	TCATGGGCT
P D P A	L M G T E G A G V	V T A T G P G V	T H L A P G D R V	M G L					
24800									
GCTCTCGGC	GCGTACGCC	CGGTGTCGT	GGCGACGCG	CGGACCGTCG	CGCGATGCC	CGAGGGGTGG	ACGTTGCCC	AGGCGCCTC	CGTGCCGGTG
L S G A	Y A P V V V A D A	R T V A R M P	E G W T F A Q	G A S V P V					
24900									
GTGTTCTGA	CGGCCGTCTA	CGCCCTGCG	GACTGGCGG	ACGTCAAGC	CGGCGAGCG	CTCCTGGTCC	ACTCCGCGC	CGGTGGCGTG	GGCATGGCCG
V F L T	A V Y A L R D L A D	V K P G E R L L V H	S A A G G V G M A	A					
25000									

FIG. 31XX

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CGGTGCAGCT	CGCCCGGCAC	TGGGGCGTGG	AGGTCACGG	CACGGCGAGT	CACGGGAAGT	GGGACGCCCT	CGCGCGCTC	GGCCTGGAGC	ACGGCACAT
V Q L	A R H	W G V	E V H	G T A S	H G K W	D A L	R A L	G L D	D A H I
CGCTCCTCC	CGACCCCTGG	ACTTCGAGTC	CGCGTTCGGT	CGCGCTTCCG	CGGGGCGGG	CATGGACGTC	GTACTGAACT	CGCTCGCCCG	CGAGTTGTC
A S S	R T L	D F E	S A F	R A A S	G G A G	M D V	V L N	S L A	R E F V
GAGCCCTCGC	TGCGCTGCT	CGGGCCGGGC	GGCCGGTTCG	TGGAGATGG	GAAGACCGAC	GTCCGCGACG	CGGAGCGGT	CGCCGCGGAC	CACCCCGGTG
D A S	L R L	L G P	G G R	F V E	M G K T	D V R	D A E	R V A	A D H P G V
TCGGCTACCG	CGCCTTCGAC	CTGGGCGAGG	CCGGGCCGGA	GCGGATCGGC	GAGATGCTCG	CCGAGTCAAT	CGCCCTCTTC	GAGGACGGGG	TGCTCCGGCA
G Y R	A F D	L G E	A G P	E R I	G E M	L A E	V I A	L F E	D G V L R H
CTGCCCCGTC	ACGACTGCG	ACGTGCGCGG	GGCCCGCGAC	GCCTTCGGGC	ACGTCAGCCA	GGCCCGCCAC	ACGGGCAAGG	TGTCCTCAC	GATGCCGTCG
L P V	T T W	D V R	R A R	D A F	R H V	S Q A	R H T	G K V	V L T M P S

FIG. 31YY

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

PmlI
▼

GGCCTCGACC CGGAGGTAC GGTCTGTCTG ACCGGCGGCA CCGGTGCGCT GGGGGGCATC GTGGCCCGGC ACCTGTGGG CGAGTGGGC GTACGACGCC 25600
G L D P E G T V L L T G G T G A L G G I V A R H V V G E W G V R R L

ApaLI
▼

TGCTGCTCGT GAGCCGGCGG GGCACGGACG CCCCGGGCGC CCGGAGCTC GTGCACGAGC TGGAGGCCCT GGGAGCCGAC GTCTCGGTGG CCGCGTGC GA 25700
L L V S R R G T D A P G A G E L V H E L E A L G A D V S V A A C D

CGTCGCCGAC CGCGAAGCCC TCACCGCGCT ACTCGACTCG ATCCCGCGCG AACACCCGCT CACCGCGGTC GTCCACACGG CAGGCGTCCT CTCCGACGGC 25800
V A D R E A L T A V L D S I P A E H P L T A V V H T A G V L S D G

ACCTCCCTT CGATGACAGC GGAGGATGTG GAACACGTAC TGGCTCCCAA GGTCGACGCC GCGTTCCTCC TCGACGAACT CACCTCGACG CCGGGCTACG 25900
T L P S M T A E D V E H V L R P K V D A A F L L D E L T S T P G Y D

ACCTGGCAGC GTTCGTCATG TTCTCCTCCG CCGCCGCCGT CTTCTGTGGC GCGGGGCAGG GCGCCTACGC CGCCGCGCAAC GCCACCCCTCG ACGCCCTCGC 26000
L A A F V M F S S A A A V F G G A G Q G A Y A A A N A T L D A L A

FIG. 31ZZ

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CTGCGCGCGC CGACAGCCG GACTCCCGC CCTCTCCCTC GGCTGGGGCC TCTGGCCGA GACCAGCGC ATGACCGCG GACTCAGCGA CACCGACCGC 26100
 W R R R T A G L P A L S L G W G L W A E T S G M T G G L S D T D R

TGCGCGCTGG CCCGTCGG GCGAGCGCC ATGACAGCG AGCTGACCCT GTCCCTCCTG GACGCGGCA TCGCGCGGA CGACCCGGCG CTCGTCCGA 26200
 S R L A R S G A T P M D S E L T L S L L D A A M R R D D P A L V P I

TGCGCCTGGA CGTCGCGCG CTCGCGGCC AGCAGCGGA CGGCATGCTG GCGCGCTGC TCAGCGGCT CACCGCGGA TCGCGGTCG GCGCGCGCC 26300
 A L D V A A L R A Q Q R D G M L A P L L S G L T R G S R V G G A P

EspI SphI Bpu1102I AscI
 ▼ ▼ ▼ ▼

GGTCAACCG CGCAGGGCAG CCGCGCGAG CGCGGGCGAG ACCTCGCGG GCGGTCGCC GCGATGACAC CGGACGACCG GGTCGCGCAC 26400
 V N Q R R A A A G G A G E A D T D L G G R L A A M T P D D R V A H

PmlI
 ▼

CTGCGGGACC TCGTCGTAC GCACGTGGG ACCGTCTCTG GACACGGCAC CCCGAGCGG GTGACCTGG AGCGGGCCTT CCGGACACCG GGTTCGACT 26500
 L R D L V R T H V A T V L G H G T P S R V D L E R A F R D T G F D S

FIG. 31AAA

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CGCTCACCGC	CGTCGAATC	CGCAACGTC	TCAACGCC	GACCGGCTG	CGGCTGCCG	CCACGCTGGT	CTTCGACCAC	CCCACCCCGG	GGGAGCTCGC
L T A	V E L	R N R L	N A A	T G L	R L P A	T L V	F D H	P T P G	E L A
CGGGCACCTG	CTCGACGAAC	TGCGCACGCG	CGCGGGCGGG	TCCTGGGCGG	AAGGCACCG	GTCCGGGAGAC	ACGGCTCGG	CGACCGATCG	GCAGACCACG
G H L	L D E L	A T A	A G G	S W A	E G T	G S G D	T A S A	T D R	Q T T
GGGGCCCTCG	CCGAACTCGA	CCGGCTGGAA	GGCGTGCTCG	CCTCCCTCGC	GCCCGCCGCC	GGCGGCCGTC	CGGAGCTCGC	CGCCCGGCTC	AGGGCGTGG
A A L	A E L D	R L E	G V L A	S L A	P A A	G G R P	E L A	A R L	R A L A
BstXI ▼									
CCGCGGCCCT	GGGGGACGAC	GGCGACGACG	CCACCGACCT	GGACGAGGCG	TCCGACGACG	ACCTCTTCTC	CTTCATCGAC	AAGGAGCTGG	GGGACTCCGA
A A L	G D D	G D D A	T D L	D E A	S D D	D L F S	F I D	K E L G	D S D
CTTCTGACCT	GCCCGACACC	ACCGGCACCA	CCGGCACCCAC	CAGCCCCCCT	CACACACGGA	ACACGGAACG	GACAGGCGAG	ACCGGGAGCC	ATGGCGAACA
F								M A N	N

FIG. 31BBB

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

PstI
 SfiI

ACGAAGACAA GCTCCGGGAC TACCTCAAGC GCGTCACCGC CGAGCTGCAG CAGAACACCA GCGTCTGCG CGAGATCGAG GGACGCACGC ACGAGCGGT 27100
 E D K L R D Y L K R V T A E L Q Q N T R R L R E I E G R T H E P V

GGCGATCGTG GGCATGGCCT GCCGCTGCC GGGCGGTGTC GCCTCGCCG AGGACCTGTG GCAGCTGGTG GCCGGGACG GGGACCGGAT CTCGGAGTTC 27200
 A I V G M A C R L P G G V A S P E D L W Q L V A G D G D A I S E F

MluI

CCGCAGGACC GCGGCTGGGA CGTGGAGGGG CTGTACGACC CCGACCCGGA CCGTCCGGC AGGACGTACT GCCGTCGGG CGGATTCCTG CACGACGCCG 27300
 P Q D R G W D V E G L Y D P D P D A S G R T Y C R S G G F L H D A G

GCGAGTTCGA CGCCGACTTC TTCCGGATCT CGCCGCGCGA GGCCCTCGCC ATGGACCCGC AGCAGCGACT GTCCCTCACC ACCGCGTGG AGCGATCGA 27400
 E F D A D F F G I S P R E A L A M D P Q Q R L S L T T A W E A I E

GAGCGGGGC ATCGACCCGA CGGCCCTGAA GGGCAGCGGC CTCGGGTCT TCGTCGGCG CTGGCACACC GGCTACACT CGGGGCAGAC CACCGCCGTG 27500
 S A G I D P T A L K G S G L G V F V G G W H T G Y T S G Q T T A V

FIG. 31CCC

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CAGTCGCCCC	AGCTGGAGGG	CCACCTGGTC	AGCGGCGCGG	CGCTGGGCTT	CCTGTCCGGC	CGTATCGCGT	ACGTCCTCGG	TACGGACGGA	CCGGCCCTGA
Q S P E L E G H L V S G A A L G F L S G R I A Y V L G T D G P A L T									
27600									
CGGTGGACAC	GGCCTGCTCG	TCCTCGCTGG	TGCGCCCTGCA	CCTCGCGGTG	CAGGCCCTCC	GCAAGGGCGA	GTGGACATG	GCCCTCGCG	GTGGTGTAC
V D T A C S S S L V A L H L A V Q A L R K G E C D M A L A G G V T									
27700									
GGTCATGCCC	AACGGGACC	TGTTGCTGCA	GTTCAGCCGG	CAGCGCGGC	TGGCCGCGA	CGGCCGCTCG	AAGCGTTTCG	CCACCTCGGC	GGACGGCTTC
V M P N A D L F V Q F S R Q R G L A A D G R S K A F A T S A D G F									
27800									
GGCCCCGGG	AGGCGCCGG	AGTCCTGCTG	GTGGAGCGCC	TGTCGACGC	CCGCCGCAAC	GGACACCGA	TCCTCGCGGT	CGTCCGCGC	AGCGCGTCA
G P A E . G A G V L L V E R L S D A R R N G H R I L A V V R G S A V N									
27900									
ACCAGGACGG	CGCCAGCAAC	GGCCTCACGG	CTCCGCACGG	GCCCTCCAG	CAGCGCGTCA	TCCGACGGC	CCTGGCGGAC	GCCCGGCTCG	CGCCGGGTGA
Q D G A S N G L T A P H G P S Q Q R V I R R A L A D A R L A P G D									
28000									

XmnI



BamHI



FIG. 31DDD

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CGTGGACGTC	GTCGAGGCGC	ACGGCACGGG	CACGGGGCTC	GGCGACCCGA	TCGAGGCGCA	GGCCCTCATC	GCCACCTACG	GCCAGGAGAA	GAGCAGCGAA
28100	V D V	V E A	H G T	G T R	L G D	P I E	A Q A	L I A	T Y G
Q P L	R L G	A L K	S N I	G H T	Q A A	A G V	I K M	V Q A	M R H
28200	CAGCCGCTGA	GGCTGGGCGC	GTTGAAGTCG	AACATCGGGC	ACACGCAGGC	CGCGGCCCGT	GTCGCAAGTG	TCATCAAGAT	GGTCAGGCG
28300	GACTGCTGCC	GAAGACGCTG	CACGTGCGACG	AGCCCTCGGA	CCAGATCGAC	TGGTCGGCGG	GCACGGTGGG	ACTCCTCACC	GAGGCCGTCG
28400	K Q D	G G L	R R A	A V S	S F G	I S G	T N A	H V V	L E E
28500	TCGCCGGCCG	TCGAGCCGCC	GGCCGGTGGC	GGTGTGGTGC	CGTGGCCGGT	GTCGCGGAAG	ACTCCGGCCG	CGCTGGACGC	CCAGATCGGG
28600	S P A	V E P	P A G	G G V	V P W	P V S	A K T	P A A	L D A
28700	Q I G	Q L A	A						

FIG. 31EEE

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

BamHI
▼

CGGTACGCGGA CGGTCTGACG GACGTGGATC CGGCGGTGGC CGCCCGCGCC CTGTGCGACA GCCGTACGGC GATGGAGCAC CGGTCGGTCG CGGTCTGCTCTT 28600
Y A D G R T D V D P A V A A R A A R A L V D S R T A M E H R A V A V G D

CAGCCGGGAG GCACTGCGGG AGGCCCTGCG GATGCCGGA GGA CTGGTAC GCGCAGCTC CTCGGACGTG GGCCGGGTGG CGTTCGTCTT CCCCGGCCAG 28700
S R E A L R D A L R M P E G L V R G T S S D V G R V A F V F P G Q

BsmI
▼

GGCAGCAGT GGGCCGGCAT GGGCGCCGAA CTCCTTGACA GCTCACCAGA GTTCGCTGCC TCGATGGCCG AATGGAGAC CGCGCTCTCC CGCTACGTCTG 28800
G T Q W A G M G A E L L D S S P E F A A S M A E C E T A L S R Y V D

ACTGGTCTCT TGAAGCCGTC GTCCGACAGG AACCCGGCGC ACCCAGCTC GACCGCGTCG ACGTCGTCCA GCCCGTGACC TTCGCTGTCA TGGTCTCGCT 28900
W S L E A V V R Q E P G A P T L D R V D V V Q P V T F A V M V S L

ApaLI
▼

GGCGAAGGTC TGGCAGCACC ACGGCATCAC CCCCAGGCC GTGTCGGCC ACTCGCAGG CGAGATCGCC GCCCGGTACG TCGCCGGTGC ACTCACCTC 29000
A K V W Q H H G I T P Q A V V G H S Q G E I A A A Y V A G A L T L

FIG. 31FFF

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GACGACGCCG	CCCGCGTGGT	CACCTGCGC	AGCAAGTCCA	TGCGCGCCCA	CCTCGCCGGC	AAGGGCGGCA	TGATCTCCCT	CGCCCTCGAC	GAGGCGGCCG
D D A A	R V V T	L R S K S I	A A H L A G	K G G M I S	L A L D	E A A V			
TCCTGAAGCG	ACTGAGCGAC	TTGACGGAC	TCTCCGTGCG	CGCCGTCAC	GGCCCCACCG	CCACCGTGGT	CTCCGGCGAC	CCGACCCAGA	TCGAGGAAT
L K R L	S D F D	G L S V A A	V N G P T A	T V V S G D	P T Q I	E E L			
CGCCCGCACC	TGCGAGGCCG	ACGGCGTCCG	TGCGGGGATC	ATCCCGGTGG	ACTACGCCTC	CCACAGCCGG	CAGGTCGAGA	TCATCGAGAA	GGAGCTGGCC
A R T C	E A D G	V R A R I I	P V D Y A S	H S R Q	V E I I	E K E L A			
GAGGTCCTCG	CCGACTCGC	CCCGCAGGCT	CCGACGTGC	CGTTCTTCTC	CACCCCTCGAA	GGCAGCTGGA	TCACCGAGCC	GGTGTCTGAC	GGCACCTACT
E V L A	G L A P	Q A P H	V P F F S T	L E G T W I	T E P V L D	G T Y W			
GGTACCGCAA	CCTGGGCCAT	CGCGTGGGCT	TGCGCCCGCG	CGTGGAGACC	TTGGCGGTG	ACGGTTTAC	CCACTTCATC	GAGGTCAGCG	CCCACCCCGT
Y R N L	R H R V	G F A P A V	E T L A V D	G F T H F I	E V S A	H P V			

KpnI

Acc65I

▼

PmlI

▼

FIG. 31GGG

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CCTCACCATG	ACCCTCCCG	AGACCGTCAC	CGGCTTCGGC	ACCCTCCGCC	GCGAACAGGG	AGGCCAGGAG	CGTCTGGTCA	CCTCACTCGC	CGAAGCCTGG
L T M	T L P E	T V T	G L G	T L R R	E Q G	G Q E	R L V T	S L A	E A W
39600									
GCCAACGGCC	TCACCATCGA	CTGGGCGGCC	ATCCTCCCA	CCGCAACCGG	CCACACCCC	GAGCTCCCCA	CCTACGCCTT	CCAGACCGAG	CGCTTCTGGC
A N G L	T I D	W A P	I L P T	A T G	H H P	E L P T	Y A F	Q T E	R F W L
29700									
TGCAGAGCTC	CGGCGCCACC	AGCGCGCCG	ACGACTGGCG	TTACCGCGTC	GAGTGAAGC	CGCTGACGGC	CTCCGGCCAG	GCGGACCTGT	CCGGGCGGTG
Q S S	A P T	S A A	D W R	Y R V	E W K P	L T A	S G Q	A D L S	G R W
29800									
GATCGTCGCC	GTCCGGGAGCG	AGCCAGAAGC	CGAGCTGCTG	GGCGGCTGA	AGGCCGCGGG	AGCGGAGGTC	GACCTACTGG	AAGCCGGGGC	GGACGACGAC
I V A	V G S E	P E A	E L L	G A L K	A A G	A E V	D V L E	A G A	D D D
29900									
CGTGAGGCCC	TCGCGGCGCCG	GTCACCGCA	CTGACGACCG	GCGACGGCTT	CACCGGCGTG	GTCTCGCTCC	TCGACGACCT	CGTGCCACAG	GTGCGCTGGG
R E A L	A A R	L T A	L T T G	D G F	T G V	V S L L	D D L	V P Q	V A W V
30000									

FIG. 31HHH

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pkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
TGCAGGCACT	CGGGACGCC	GGATCAAGG	CGCCCTGTG	GTCCGTCACC	CAGGGCGCGG	TCTCCGTGG	ACGTCTCGAC	ACCCCGCGCG	ACCCGACCG
Q A L G D A	G I K A	P L W S V T	Q G A V	S V G R L D	T P A D	P D R			
GGCCATGCTC	TGGGGCCTCG	GCCGCTCGT	CGCCCTTGAG	CACCCCGAAC	GCTGGCGCGG	CCTCGTCGAC	CTCCCGCGCC	AGCCCGATGC	CGCGCCCTC
A M L W G L G	R V V A L E	H P E R W A G	L V D L P A Q	P D A A A L					
BsaBI									
GGCCACCTCG	TCACCGCACT	CTCCGGCGCC	ACGGCGGAGG	ACCAGATCGC	CATCCGCACC	ACCGGACTCC	ACGCGCGCGG	CCTCGCGCGC	GCACCCCTCC
A H L V T A L	S G A T G E D	Q I A I R T	T G L H A R R	L A R A P L H					
ACGACGTCG	GCCACCCGC	GACTGGCAGC	CCCACGGCAG	CGTCCTCATC	ACGGCGGCGA	CCGGAGCCCT	CGGCAGCCAC	GCCGACGCT	GGATGGCCCA
G R R P T R	D W Q P H G T	V L I T G G T	G A L G S H A A R W	M A H					
CCACGGAGCC	GAACACCTCC	TCCTCGTCAG	CCGACGGCGC	GAACAAGCCC	CCGGAGCCAC	CCAACTCACC	GCCGAACTCA	CCGCATCGGG	CGCCCCGCTC
H G A E H L L	L L V S R S G	E Q A P G A T	Q L T A E L T	A S G A R V					

FIG. 31III

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pkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
ACCATCGCCG	CCTGCGACGT	CGCCGACCCC	CACGCCATGC	GCACCCCTCCT	CGACGCCATC	CCCGCCGAGA	CGCCCCCTCAC	CGCCGTCGTC	CACACCGCCG
30600	T I A A	C D V A	D P H A	M R T L	L D A I	P A E T	P L T A	V V H T	A G
CGGCACCGGG	CGGCGATCCG	CTGGACGTCA	CGGGCCCGGA	GGACATCGCC	CGCATCCTGG	GCGGAAGAC	GAGCGGCGCC	GAGTCCTCG	ACGACCTGCT
30700	A P G G	D P L D	V T G P	E D I A	R I L G	A K T S	G A E V	L D D L	L
CCGCGGCACT	CCGCTGGACG	CCTTCGTCTT	CTACTCCTCG	AACGCCGGG	TCTGGGGCAG	CGGCAGCCAG	GGGTCCTACG	CGGCGGCCAA	CGCCCCACCTC
30800	R G T P	L D A F	V L Y S	S N A G	V W G S	G S Q G	V Y A A	A N A H	L
									MluI
									▼
GACGCGCTCG	CCGCCCGCGG	CCGCGCCCGG	GCGAGACGG	CGACCTCGGT	CGCCTGGGGC	CTCTGGGCGG	GCGACGGCAT	GGGCGGGGCG	GCGACGACG
30900	D A L A	A R R A	R R G E	T A T S	V A W G	L W A G	D G M G	R G A D	D A
									MscI
									BalI
									▼
CGTACTGGCA	GGCTGCGGGC	ATCCGTCCGA	TGAGCCCCGA	CCGGCCCTTG	GACGAATGG	CCAAGGCCCT	GAGCCACGAC	GAGACCTTCG	TCGCCGTGGC
31000	Y W Q R	R R G I	R P M S	P D R A	L D E L	A K A L	S H D E	T F V A	V A

FIG. 31JJJ

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CGATGTCGAC TGGGAGCGGT TCGCGCCCGC GTTCACGGTG TCCCGTCCCA GCCTTCTGCT CGACGGCGTC CCGGAGGCC GGCAGGCGT CGCCGCACCC 31100
D V D W E R F A P A F T V S R P S L L L D G V P E A R Q A L A A P

GTCGGTGCCC CGGCTCCCGG CGACGCCCGC GTGGGCCGGA CCGGGCAGTC GTGGCGGCTG GCCGCGATCA CCGCGCTCCC CGAGCCGAG CGCCGGCCGG 31200
V G A P A P G D A A V A P T G Q S S A L A A I T A L P E P E R R P A

CGCTCCTCAC CCTCGTCGGT ACCCAGCGG CGGCGTACT CGGCCATTCC TCCCCCGACC GGGTGGCCC CCGCGGTGCC TTCACGAGC TCGGCTTCGA 31300
L L T L V R T H A A A V L G H S S P D R V A P G R A F T E L G F D

CTCGCTGACG GCCGTGCAGC TCCGCAACCA GCTCTCCAG GTGGTCGGCA ACAGGCTCCC CGCCACCAG GTCTTCGACC ACCGACGCC CGCCGCATC 31400
S L T A V Q L R N Q L S T V V G N R L P A T T V F D H P T P A A L

GCCGCGCACC TCCACGAGC GTACCTCGCA CCGGCGGAG CCGCCCCGAC GGACTGGGAG GGGCGGTGC GCCGGGCCCT GGCCGAACTG CCCCTCGACC 31500
A A H L H E A Y L A P A E P A P T D W E G R V R A L A E L P L D R

FIG. 31KKK

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pkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GGCTGCGGGA	CGCGGGGTC	CTCGACACCG	TCCTGCGCCT	CACCGGCATC	GAGCCCGAGC	CGGTTCCGG	CGGTTCCGAC	GGCGGCGCCG	CGGACCCCTGG
L R D	A G V	L D T V	L R L	T G I	E P E	P G S G	G S D	G G A	A D P G
TGCGGAGCCG	GAGGCTCGA	TCGACGACCT	GGACGCCGAG	GCCCTGATCC	GGATGGCTCT	CGGCCCCCGT	AACACCTGAC	CCGACCGCGG	TCCTGCCCCA
A E P	E A S I	D D L	D A E	A L I	R M A	L G P	R N T		
CGCGCCGCAC	CCCGCGCATC	CCGCGCACCA	CCCGCCCCCA	CAGCCCCACA	ACCCCATCCA	CGAGCGGAAG	ACCACACCCA	GATGACGAGT	TCCAACGAAC
								M T S	S N E Q
ACTTGGTGGA	CGCTCTGCGC	GCCTCTCTCA	AGGAGAACGA	AGAACTCCGG	AAAGAGAGCC	GTGCGCGGCG	CGACCGTCGG	CAGGAGCCCCA	TGGCGATCGT
L V D	A L R	A S L	K E N	E E L	R K E	S R R	R A D	R R Q	E P M A I V
CGGCATGAGC	TGCCGGTTCG	CGGGCGGAAT	CCGTCCTCCC	GAGGACCTCT	GGGACGCCGT	CGCCGCGGCG	AAGGACCTGG	TCTCCGAGGT	ACCGGAGGAG
G M S	C R F	A G G	I R S	P E D	L W D	A V A	A G K	D L V	S E V P E E

KpnI
Acc65I

FIG. 31LLL

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CGCGGCTGGG	ACATCGACTC	CCTCTACGAC	CCGCTGCCCC	GGCGCAAGGG	CACGACGTAC	GTCGCAACG	CCGCGTTCCT	CGACGACGCC	GCCGGATTGG
R G W D	I D S	L Y D	P V P G	R K G	T T Y	V R N A	A F L	D D A	A G F D
ACGCGGCCTT	CTTCGGGATC	TCGCCGCGCG	AGGCCCTCGC	CATGGACCCG	CAGCAGCGGC	AGCTCCTCGA	AGCCTCCTGG	GAGGTCTTCG	AGCGGGCCCG
A A F	F G I	S P R E	A L A	M D P	Q Q R Q	L L E	A S W	E V F	E R A G
CATCGACCCC	GCCTCGGTCC	GCGGCACCGA	CGTCGGCGTG	TACGTGGGCT	GTGCTACCA	GGACTACGG	CCGGACATCC	GGGTGCCCC	CGAAGGCACC
I D P	A S V R	G T D	V G V	Y V G C	G Y Q	D Y A	P D I R	V A P	E G T
GGCGGTACG	TCGTCACCGG	CACTCCTCC	GCCGTGGCCT	CCGGCGCAT	CGCGTACTCC	CTCGGCTTG	AGGGACCCGC	CGTGACCGTG	GACACGGCGT
G G Y V	V T G	N S S	A V A S	G R I	A Y S	L G L E	G P A	V T V	D T A C
GCTCCTCTTC	GCTCGTCGCC	CTGCACCTCG	CCCTGAAGGG	CCTGCGGAAC	GGCGACTGCT	CGACGGCACT	CGTGGGCGGC	GTGGCCGTCC	TCGCGACGCC
S S S	L V A	L H L A	L K G	L R N	G D C S	T A L	V G G	V A V	L A T P

FIG. 31MMM

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plPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GGGCGGTTTC	ATCGAGTTCA	GCAGCCAGCA	GGCCATGGCC	GCCGACGGCC	GGACCAAGGG	CTTCGCTCG	GCGGCGGACG	GCCTCGCCTG	GGGCGAGGGC
G A F	I E F S	S Q Q	A M A	A D G R	T K G	F A S	A A D G	L A W	G E G
32600									
GTGCGCGTAC	TCCTCCTCGA	ACGGCTCTCC	GACGGGCGGC	GCAAGGGCCA	CCGGTCTCTG	GCCGTCTGTC	GCGGACGGCG	CATCAACCAG	GACGGCGCGA
V A V L	L L E	R L S	D A R R	K G H	R V L	A V V R	G S A	I N Q	D G A S
32700									
GCAACGGCCT	CACGGCTCCG	CACGGGCCCT	CCGACGAGCA	CCTGATCCGC	CAGGCCCTGG	CCGACGGCGG	GCTCAGCTCG	AGCGACGTGG	ACGTCGTGGA
N G L	T A P	H G P S	Q Q H	L I R	Q A L A	D A R	L T S	S D V D	V V E
32800									
GGGCCACGGC	ACGGGACCC	GTCTCGGCGA	CCCGATCGAG	GCGCAGGCGC	TGCTCGCCAC	GTACGGGCAG	GGGCGCGCCC	CGGGGACGCC	GCTGCGGCTG
G H G	T G T R	L G D	P I E	A Q A	L L A T	Y G Q	G R A P	G Q P	L R L
32900									
GGGACGCTGA	AGTCGAACAT	CGGGCACACG	CAGGCCGCTT	CGGGTGTGCG	CGGTGTTCATC	AAGATGGTGC	AGGCGCTGCG	CCACGGGGTG	CTGCCGAAGA
G T L K	S N I	G H T	Q A A S	G V A	G V I	K M V	Q A L R	H G V	L P K T
33000									

Asci
▼

FIG. 31NNN

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

PmlI

▼
 CCTGACGT GGAGAGCG ACGACCAGG TCGACTGGT GGGCGGTTG GTCGAGTGC TCACCGAGC CGTGGACTGG CCGGAGCGGC CGGGCCCGCT 33100
 L H V D E P T D Q V D W S A G S A G S V E L L T E A V D W P E R P G R L

CCGCCGGCG GCGTCTCCG CGTTCGGCGT GGGCGGAGC AACCGGCACG TCGTCTGGA GGAGGCCCG GCGGTCGAG AGTCCCCTGC CGTCGAGCG 33200
 R R A G V S A F G V G G T N A H V V L E E A P A V E E S P A V E P

CCGCCCGGT GCGGCTGGT GCGTGGCG AGACTCGGC CGACTGGAC GCCAGATCG GGCAGCTGC CGCATACGCG GAAGACCGCA 33300
 P A G G G V V P W P V S A K T S A A L D A Q I G Q L A A Y A E D R T

BamHI

▼
 CGGACGTGA TCCGGCGTG GCCGCCCGC CCTGGTGA CAGCGTACG GCGATGAGC ACCGCGGT CGCGTGGC GACAGCCGG AGGCACTGC 33400
 D V D P A V A A R A L V D S R T A M E H R A V A V G D S R E A L R

GGACGCCCTG CGGATGCCG AAGACTGGT ACGGGGCAG GTCACGATC CCGGCCGGT GCGTTCGTC TTCCCCGCC AGGGCACGCA GTGGCCCGC 33500
 D A L R M P E G L V R G T V T D P G R V A F V F P G Q G T Q W A G

FIG. 31000

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pikPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

EcoRI
 ApoI

BsmI

ATGGGCGCG AACTCCTCGA CAGCTCACCC GAATTCGCCG CCGCCATGGC CGAATGCGAG ACCGCACTCT CCCCGTACGT CGACTGGTCT CTCGAAGCCG 33600
 M G A E L L D S S P E F A A A M A E C E T A L S P Y V D W S L E A V

TCGTCCGACA GGCTCCCGAG GCACCGACAC TCGACCGCGT CGACGTCGTC CAGCCCGTCA CCTTCGCGGT CATGGTCTCC CTGCGCAAGG TCTGGCAGCA 33700
 V R Q A P S A P T L D R V D V V Q P V T F A V M V S L A K V W Q H

CCACGGCATC ACCCCCGAGG CCGTCATCGG CCACTCCGAG GCGAGATCG CCGCCGCGTA CGCTCACCC TCGACGACGC CGCTCGTGTC 33800
 H G I T P E A V I G H S Q G E I A A A Y V A G A L T L D D A A R V

GTGACCTCC GCAGCAAGTC CATCGCCGCC CACCTCGCCG GCAAGGCGG CATGATCTCC CTCGCCCTCA GCGAGGAAGC CACCCGGCAG CGCATCGAGA 33900
 V T L R S K S I A A H L A G K G G M I S L A L S E E A T R Q R I E N

ACCTCCACGG ACTGTGATC GCGCCGTCA ACGGGCCTAC CGCCACCGTG GTTTCGGGGG ACCCCACCCA GATCCAAGAA CTGCTCAGG CGTGTGAGGC 34000
 L H G L S I A A V N G P T A T V V S G D P T Q I Q E L A Q A C E A

FIG. 31PPP

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CGACGGCATC CGCGCACGGA TCATCCCCGT CGACTACGCC TCCACACGCG CCCACGTGGA GACCATCGAG AACGAACCTCG CCGACGTCCT GGCGGGGTTG 34100
D G I R A R I I P V D Y A S H S A H V E T I E N E L A D V L A G L

KpnI
▼
Acc65I
▼

TCCCCCCAGA CACCCAGGT CCCCTTCTTC TCCACCTCG AAGGACCTG GATCACGGA CCCGCCCTCG ACGGCGGCTA CTGGTACCGC AACCTCGCC 34200
S P Q T P Q V P F F S T L E G T W I T E P A L D G G Y W Y R N L R H

ATCGTGTGGG CTTGCGCCCG GCGTTCGAGA CCTCGGCCAC CGACGAAGGC TTCACCCACT TCATCGAGGT CAGCGCCAC CCGTCTCTCA CCATGACCT 34300
R V G F A P A V E T L A T D E G F T H F I E V S A H P V L T M T L

MscI
BclI
▼

CCCCGACAAAG GTACCGGCC TGGCCACCCT CCGACGCGAG GACGGCGGAC AGCACCGCT CACCACCTCC CTGCGGAGG CTGGGGCCAA CGGCCTCGCC 34400
P D K V T G L A T L R R E D G G Q H R L T T S L A E A W A N G L A

CTCGACTGGG CCTCCCTCCT GCCGCGCAGG GCGGCCCTCA GCCCGCGCGT CCCGACCTC CCGACGTAG CCTTCCAGCA CCGCTCGTAC TGGATCAGCC 34500
L D W A S L L P A T G A L S P A V P D L P T Y A F Q H R S Y W I S P

FIG. 31QQQ

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pikPKS Sequence

[illegible]

CCGCGGGTCC CGCGGAGGCG CCGCGGCACA CCGTTTCGG GCGGAGGCC GTCGCCGAGA CCGGGCTCGC GTGGGGCCG GGTGCCGAGG ACCTCGACGA 34600
A G P G E A P A H T A S G R E A V A E T G L A W G P G A E D L D E

GGAGGGCCGG CGCAGGCCG TACTCGCAT GGTGATCGG CAGGCGGCCT CCGTCTCCG GTGGACTCG CCCGAGAGG TCCCCGTGA CGCCCGCTG 34700
E G R R S A V L A M V M R Q A A S V L R C D S P E E V P V D R P L

CGGGAGATCG GCTTCGACTC GTGACCGCC GTGACTTCC GCAACCGGT CAACCGGCTG ACGGTCTCC AGTGGCGCC CACCGTCGTG TTCCAGCAC 34800
R E I G F D S L T A V D F R N R V N R L T G L Q L P P T V V F Q H P ACP 6 *

CGACGCCCGT CGGCTCGCC GAGCGCATCA GCGACGAGCT GGCCGAGCGG AACTGGGCGG TGGCCGAGCC GTGGATCAC GAGCAGGCGG AGGAGGAGAA 34900
T P V A L A E R I S D E L A E R N W A V A E P S D H E Q A E E K
→ TE domain

GGCCGCGCGT CCGCGGGGG CCGGTCGG GCGGACACC GCGCGCGG CCGGATGTT CCGCGCAGG CCGTGGAGG CGACCGTAC 35000
A A A P A G A R S G A D T G A G A G M F R A L F R Q A V E D D R Y

FIG. 31RRR

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

GGCGAGTTCC TCGACGTCCT CGCCGAAGCC TCCGGGTTC TCCCTCGCCC GAGGCCTGCT CGGAGCGGCT CGACCCGGTG CTGCTGCGCG 35100
G E F L D V L A E A S A F R P Q F A S P E A C S E R L D P V L L A G

EspI
Bpu1102I
▼

GGGTCCGAC GGACCGGGCG GAAGGCCGTG CCGTTCTCGT CGGCTGCACC GGCACCGCGG CGAAGCGCGG CCGGCACGAG TTCCTGCGGC TCAGCACCTC 35200
G P T D R A E G R A V L V G C T G T A A N G G P H E F L R L S T S

CTTCCAGGAG GAGCGGACT TCCTGCGCGT ACCTCTCCCC GGCTACGGCA CGGTACGGG CACCGGCACG GCCCTCCTCC CGGCCGATCT CGACACCGCG 35300
F Q E E R D F L A V P L P G Y G T G T G T G T A L L P A D L D T A

CTCGACGCC AGGCCCGGC GATCTCCGG GCCCGCGGG AGCCCCGGT CGTCTGCTC GGGCGGCCCT GCTCGCGCAC GAGCTGGCCT 35400
L D A Q A R A I L R A A G D A P V V L L G H S G G A L L A H E L A F

AscI
▼

TCCGCTTGA GCGGGCGCAC GCGCGCGCG GCGCGGGGAT CGTCTGCTC GACCCCTATC CGCCGGGCCA TCAGGAGCCC ATCGAGGTGT GGAGCAGGCA 35500
R L E R A H G A P P A G I V L V D P Y P P G H Q E P I E V W S R Q

FIG. 31SSS

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

MscI
BamI

GCTGGGCGAG GGCCTGTTCG CGGGCGAGCT GGAGCCGATG TCCGATGCGC GGCTGCTGGC CATGGGCCGG TACGGCGGGT TCCTGCGCGG CCGGCGGCCG 35600
L G E G L F A G E L E P M S D A R L L A M G R Y A R F L A G P R P

GGCGGCAGCA GCGCGCCCGT GCTTCTGGTC CGTGGCTCCG AACCGCTGGG CGACTGGCAG GAGGAGCGGG GCGACTGGCG TGCCCACTGG GACCTTCCGC 35700
G R S S A P V L L V L L V R A S E P L G D W Q E E R G D W R A H W D L P H

ACACCGTCGC GGACGTGCGG GCGGACCACT TCACGATGAT GCGGGACCAC GCGCGGCCG TCGCCGAGGC CGTCTCTCC TGGCTCGACG CCATCGAGGG 35800
T V A D V P G D H F T M M R D H A P A V A E A V L S W L D A I E G

BamHI

CATCGAGGGG GCGGGCAAGT GACCGACAGA CCTCTGAACG TGGACAGCG ACTGTGGATC CGGCGCTTCC ACCCGCGCC GAACAGCGCG GTGCGGCTGG 35900
I E G A G K V T D R P L N V D S G L W I R R F H P A P N S A V R L V
→

TE2

TTTGCCTGCC GCACGCCGGC GGCTCCGCCA GCTACTTCTT CCGCTTCTCG GAGGAGTGC ACCCTCCGT CGAGGCCCTG TCGGTGCACT ATCCGGGCCG 36000
C L P H A G G S A S Y F F R F S E E L H P S V E A L S V Q Y P G R

FIG. 31TTT

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plPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890

CCAGGACCGG CGTGCCGAGC CGTGCTGGA GAGCTGCGG GAGCTGTGGT CGCGGCCACC GAACCTGGT GGCAGGAGGG CCGGCTGGCC 36100

Q D R R A E P C L E S V E E L A E H V V A A T E P W W Q E G R L A

TTCTTCGGC ACAGCTCGG CGCTCCGTC GCCTTCGAGA CGGCCCGCAT CCTGGAACAG CGGCACGGGG TACGGCCCGA GGGCCTGTAC GTCTCCGTC 36200

P F G H S L G A S V A F E T A R I L E Q R H G V R P E G L Y V S G R

▼
 AscI
 EspI
 Bpu1102I

GGCGGCCCC GTCGCTGGC CCGGACCGG TCGTCCACCA GCTGGAGAC CGGCGGTTC TGGCCGAGAT CCGGCGGCTC AGCGGCACCG ACGAGCGGTT 36300

R A P S L A P D R L V H Q L D D R A F L A E I R R L S G T D E R F

CCTCCAGGAC GACGAGCTGC TCGCGCTGGT GCTGCCCGG CTGCGCAGCG ACTACAAGGC GCGGAGAGC TACCTGCACC GCGCGTCCGC CAAGCTCACC 36400

L Q D D E L L R L V L P A L R S D Y K A A E T Y L H R P S A K L T

TGCCCCGTGA TGCCCCTGGC CGGCGACCGT GACCCGAAGG CGCCGCTGAA CGAGGTGGCC GAGTGGCGTC GGCACACCAG CCGGCGCGTTC TGCCTCCGGG 36500

C P V M A L A G D R D P K A P L N E V A E W R R H T S G P F C L R A

FIG. 31UUU

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plkPKS Sequence

10	20	30	40	50	60	70	80	90	100
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
CGTACTCCGG CGGCCACTTC TACCTCAACG ACCAGTGGCA CGAGATCTGC AACGACATCT CCGACCACCT GCTCGTCACC CGCGGCGCGC CCGATGCCCG 36600									
Y S G	G H F	Y L N	D Q W	H E I	C N D I	S D H	L L V	T R G A	P D A R
CGTCGTGCAG CCCCAGACCA GCCTTATCGA AGGAGCGGCG AGAAGATGGC AGAACCCACG GTGACCGACG ACCTGACGGG GGCCCTCAGC CAGCCCCCGC 36700									
V V Q	P P T	S L I	E G A	A K R	W Q N	P R			
TGGGCGGCAC CGTCCGCGCG GTGGCGGACC GTGAATCTGG CACCCACCTC CTGGAGACCC GGCGCATCCA CTGGATCC 36778									

FIG. 31VV

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
BamHI								
▼								
GGATCCGGCGCTTCCACCCCGCGCCGAACAGCGCGGTGCGGCTGGTCTGCCCTGCCGACGCCGGCGGGCTCCGCCAGCTACTTCTCCGCT								90
CCTAGGCCGCGAAGGTGGGGCGCGGCTTGTTCGGGCCACGCCGACCAAGACGACGGCGGTGCGGCCCGCCGAGCGGTTCGATGAAGAAGCGGA								
I R R F H P A P N S A V R L V C L P H A G S A S Y F F R F								
TCTCGGAGGAGTGACCCCTCCGTCGAGGCCCTGTGCGTGCAATCCGGGCCGCCAGGACCGGCGTCCCGAGCCGCTGTCTGGAGAGCG								
AGACCTCCTCGACGTGGGGAGGACGCTCCGGGACAGCCACGTATAGCCCGCGGTCTCTGGCCGACCGGCTCGGCACAGACCTCTCGC								180
S E E L H P S V E A L S V Q Y P G R Q D R R A E P C L E S V								
NspHI								
▼								
TCGAGGAGCTCGCCGAGCATGTGGTCGGGCCACCGAACCCCTGTGGCAGGAGGCCCGGCTGGCCCTTCTTCGGGCACAGCCCTCGGCGCCT								270
AGTCCTCGAGCGGCTCGTACACAGCGCCGGTGGCTTGGACCAACCGTCTCCGGGCCGACCCGGAAGAAGCCCGTGTTCGAGCCCGCGGA								
E E L A E H V V A A T E P W Q E G R L A F F G H S L G A S								
AscI								
▼								
CCGTCCGCTTCGAGACGGCCCGCATCCTGGAAACAGCGGCACGGGGTACGGCCGAGGGCCTGTACGTCTCCGGTCCGGCGCCCCCGCTCGC								360
GGCAGCGGAAGCTCTGCCGGGCGTAGACCTTGTTCGCCGTGCCCATGCCGGCTCCCGGACATGCAGAGGCCAGCCCGCGGGGCGAGCG								
V A F E T A R I L E Q R R H G V R P E G L Y V S G R R A P S L								

FIG. 32A

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[illegible]

FIG. 32B

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
AscI ▼ TCACCCGGCGCGCCGATGCCCGCGTCGTGACGCCCGCCGACACGCTTATCGAAGGAGCGGCGAAGAGATGGCAGAAACCCACGGTGAC AGTGGCGCGCGCGGCTACGGGGCGCAGACGTCGGGGCTGGTCGGAATAGCTTCCCTCGCCGCTTCTCTACCGTCTTGGGTGCCACTG T R G A P D A R V V Q P P T S L I E G A A K R W Q N P R V T								
EarI ▼ BstEII ▼								
810								
Apal ▼ PflMI ▼								
900								
BamHI ▼								
990								
BstEII PvuII ▼								
1080								

FIG. 32C

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
123456789012345678901234567890123456789012345678901234567890								
CTCGACGGACTTCGGGGTCTCCGGCGCGACGGCGTCCGGTGCCGACAGGTCCTCTCGTACGGGGAGGGTGTCGGCTGGAGCGCGA								1170
GAGCTGCCCTGAAGCCCCAGAGGCCCGCGGTGCCGACAGGCCACGGCGTCGTCCAGGAGAGCATGCCCTCCCGACAGGCGACCTCGCGCT								
S T D F G V S G A D G V P V P Q Q V L S Y G E G C P L E R E								
AlwNI								
▼								
GCAGGTGCTCCGGCGCGGTGACGTGCCGGAGGGCGGCGAGCGTGCCGTGGTCGAGGGGATCCACCGGGAGACGCTGGAGGGTCTCGC								1260
CGTCCACGACGGCCCGCGGCCACTGCACGGCCCTCCGCCCTCCGACCGCACCGCAGCTCCCCCTAGGTGGCCCCCTCTCGACCTCCAGAGCG								
Q V L P A A G D V P E G G Q R A V V E G I H R E T L E G L A								
GCCGACCCGTCGGCGTCGTACGCCCTTCGAGCTGCTGGGCGGTTTCGTCCGCCCGCGGTGACGGCGCTGCCCGCCGCGTGTGGGTGT								1350
CGGCTGGGCAGCCGCAGCATGCGGAAGCTCGACGACCCCGCCAAAGCAGGCGGCGCCGACCTGCCGGCGACGGCGGCGCACGCCACACA								
P D P S A S Y A F E L L G G F V R P A V T A A A A V L G V								
RsrII								
▼								
TCCCGCGGACCGGCGCGGACTTCGCGGATCTGCTGGAGCGGCTCCGGCCGCTGTCCGACAGCCTGCTGGCCCCCGCAGTCCCTGCGGAC								1440
AGGGCGCCTGGCGCGCCTGAAGCGCCTAGACGACCTCGCCGAGGCCGCGGACAGGCTGTCCGACGACCGGGGCGTTCAGGGGACGCCTG								
P A D R R A D F A D L L E R L R P L S D S L L A P Q S L R T								

FIG. 32D

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
123456789012345678901234567890123456789012345678901234567890								
GGTACGGGGCGGACGGGCGGTGGCCGAGCTCACGGCGGTGCTCGCGCTCCTCGCGCATCCCGAGCAGTGGCGGGAGCTGTGCGACCGGCCCGG								1530
CCATGCCCGCCGCTGCCGCGGACCGGCTCAGTGCCTGCGGACGAGCGGCTAAGCTGTGAGGGGGCCCGGGACGACAGCCGCGAGCC								
V R A A D G A L A E L T A L L A D S D S P G A L L S A L G								
				TfiI			Apal	
				▼			▼	
BstEII								
▼								
GGTACCGGAGCGGTCCAGCTCACCGGAGACCGCGGTGCTCGCGCTCCTCGCGCATCCCGAGCAGTGGCGGGAGCTGTGCGACCGGCCCGG								1620
CCAGTGGCGTCCGACGAGTCGAGTGGCCCTTTCGCCACGAGCGCGAGGAGCGGTAGGCTCGTACCGCCCTCGACACGCTGGCCCGG								
V T A A V Q L T G N A V L A L A L A H P E Q W R E L C D R P G								
NotI								
▼								
GCTCGGGCGGCGGTGGAGGAGACCTCCGCTACGACCCCGCGGTGCTCGAGCTCGACGCCCGGTGGTCCGCGGGGAGACGGAGCTGGC								1710
CGAGCGCGCGCGCCACCTCCTCTGGGAGGCGATGCTGGGCGGCCACGTCGAGCTCGGGCCACCCAGGCGCCCTCTGCTCCTCGACCG								
L A A A A V E E T L R Y D P P V Q L D A R V V R G E T E L A								
				NspHI			BbsI	Eco47III
				▼			▼	▼
GGGCGGGCGGTGCCGGCGGGCGCATGTGCTGCTGACCGCGGACCGCGCGGACCCGAGGTCTTACGGACCCCGGAGCGCTT								1800
CCCGCGCGCGACCGCGCGCGCGGTACAGCAGGAGTGGCGGCGCTGGCGCGCCCTGGGCCCTCCAGAAGTGCCTGGGCCCTCGCGAA								
G R R L P A G A H V V V L T A A T G R D P E V F T D P E R F								

FIG. 32E

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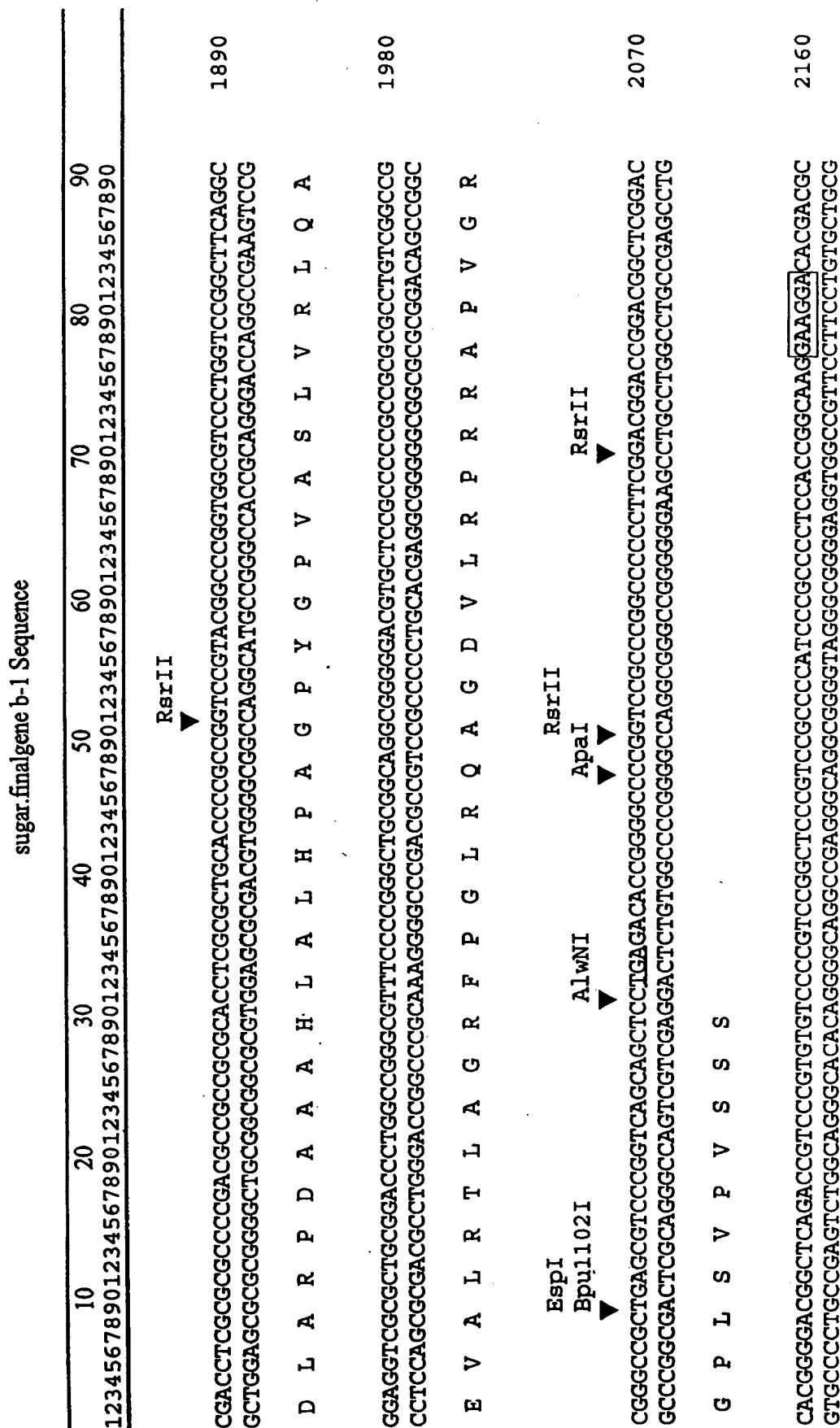


FIG. 32F

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
CATGCGGTCCTGCTGACCTCGTTGCGCACATCACACGCACCTACTACGGCCTGGTGCCTGGCCTGGCGCTGCTCGCCCGCCGGGCACGA								
GTACGCGCAGGACGACTGGAGCAAGCGTGTAGTGTGCGTGATGATGCCGACACCGGGGACCGGACCCCGCGACGAGCGGCGGCCCGTGCT								
M R V L L T S F A H H T H Y Y G L V P L A W A L L A A G H E								
2250								
DraIII								
GGTGGGGTCGCCAGCCCGGCTCACGGACACCATCACGGGTCCGGGCTCGCCGGGTCCGGTCCGGTCCGACCCGACCCACCTCATCCA								
CCACGCCCAAGCGTCCGTCGGGCGCGAGTGCCTGTGGTAGTGGCCAGGCCCGGAGCGGCCACCGCCAGCCGTCGCTGGTGGAGTAGGT								
V R V A S Q P A L T D T I T G S G L A A V P V G T D H L I H								
2340								
PvuI								
CGAGTACCGGGTGGCGGCGAGCCGCGCCGGAACCATCCGGCGATCGCCTTCGACGAGGCCCGTCCGAGCCGCTGGACTGGGA								
GCTCATGGCCCCACGCCCTACCGCCCCGCTCGGGCGCGGGCTTGGTAGGCCGCTAGCGGAAGCTGCTCCGGGACGGGCTCGGCGACCTGACCCCT								
E Y R V R M A G E P R P N H P A I A F D E A R P E P L D W D								
2430								
CCACGCCCTCGGCATCGAGGCGATCCTCGCCCCCGTACTTCCATCTGCTCGCCCAACAAACGACTCGATGGTCGACGACCTCGTCGACTTCGC								
GGTGGGGAGCCGTAGCTCCGCTAGGAGCGGGGCGATGAAGTAGACGAGCGGTTGTTGCTGAGCTACCAAGCTGCTGGAGCAGCTGAAGCG								
H A L G I E A I L A P Y F H L L A N N D S M V D D L V D F A								
2520								

FIG. 32G

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
CCGGTCC	TGGCAG	CCGGAC	CTGGTG	TGGGAG	CCGACG	ACCTAC	CGGGGG	CGCGT
GGCCAG	GACCGC	TGGACC	ACGAC	ACCC	CTCGGC	TGCTGG	ATGCGC	CGCGCG
R S W Q	P D L V	L W E P	T T Y A	G A V A	A Q V T	G A A H	A R	
2610								
GGTCCT	TGTTGG	GGCCCG	AGCGCC	CGCCCG	CAAGTT	CGTGGG	GACCGG	CAAGCC
CCAGGA	CACCCC	GGGCTG	CACTAC	CCCGT	CGCGGG	CGGTTC	AAGCAG	CGCGCC
V L W G	P D V M	G S A R	R K F V	A L R D	R Q P P	E H R E	D P	
2700								
CACCGG	AGTGCT	GACGTG	GACGCT	CGACCG	GTACGG	GCCTCCT	TCGAA	GAGAGT
GTGGCG	CCTCAC	CGACTG	CACTG	CGGCA	TGCGGC	AGTTC	CTCGAC	GAGTGG
T A E W	L T W T	L D R Y	G A S F	E E L L	T G Q F	T I D P	T	
2790								
CCGCGG	AGCCTG	CGCCTC	GACCGC	CGTGGG	ATGCTT	ATGTTCC	GTACAA	CGGACG
GGCGGC	CTCGGA	CGGAGC	TGTGCC	CGGACG	CGTGGC	ATGTTG	CCGTGC	AGCCAG
P P S L	R L D T	G L P T	V G M R	Y V P Y	N G T S	V V P D	W L	
2880								

FIG. 32H

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
123456789012345678901234567890123456789012345678901234567890								
GAGTGAGCCCGCCCGCGCCCGGGTCTGCCCTGACCCCTCGGCGGTCTCGGCGGTGAGGTCTCGGCGGCGACGGCGTCTCGCAGGGCGA								
CTCACTCGGCGGGCGCGCCCGGGCCAGACGGACTGGGAGCCGCGAGCGCGCACTCCAGGAGCCCGCGCTGCCGCGAGAGCGTCCCCGCT								
S E P P A R P A R P R V C L T L G V S A R E V L G G D G V S Q G D								
2970								
CATCCTGGAGGCGCTCGCCGACCTCGACATCGAGCTCGTGCCACGCTCGACGCGAGTCAGCGCGCCGAGATCCGGCAACTACCCGAAGCA								
GTAGGACCTCCGCGAGCGGCTGGAGCTGTAGCTCGAGCAGCGGTGCGAGCTGCGCTCAGTCGCGCGGCTCTAGGCGTTGATGGGCTTCGT								
I L E A L A D L D I E L V A T L D A S Q R A E I R N Y P K H								
3060								
CACCCGGTTACGGACTTCGTGCCGATGCA CGGCTCTCTGCCGAGCTGCTCGGCGATCATCCACCACGGCGGGCGGGCACCTAGCGGAC								
GTGGGCCAAGTGCCCTGAAGCACGGCTACGTGCGCGAGGACGGCTCGACGAGCCGCTAGTAGTGTCGCCGCCCGCGCGTGGATGCGCTG								
T R F T D F V P M H A L L P S C S A I I H H G G A G T Y A T								
3150								
BclI								
CGCCGTGATCAACGGGTGCCGAGGTGATGCTGCCGAGCTGTGGACGGCCCGGTCAAGGCGGGCGCGTCCGAGCAGGGGGCGGG								
GCGGCACTAGTTGCGCCACGGCGTCCAGTACGAGCGGCTCGACACCCCTGCGGGCCAGTTCCGCGCCCGCGCAGCGGCTCGTCCCCCGCCC								
A V I N A V P Q V M L A E L W D A P V K A R A V A E Q G A G								
3240								

FIG. 32I

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10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
GTTCCTCGCGCGCGAGCTACGCCGCGAGCGCGTGGGACGCCGTGTCGCATCCTCGACGACCCCTCGGTGCGCACCGCGCG								
CAAGAAGGACGGCGCGCGCTCGAGTGGCGCGTCCGGCACGCCCTGCGGACAGCGGTAGGAGCTGCTGGGAGCCAGCGGTGGCGGCG								
F F L P P A E L T P Q A V R D A V V R I L D D P S V A T A A								
3330								
GCACCGGCTGCGCGAGGAGACCTTCGGCGACCCCAACCGCGCGGATCGTCCCGAGCTGGAGCGGCTCGCCGCGCAGCACCGCGCGCC								
CGTGGCGGACCGCGCTCCTCTGGAAGCCGCTGGGGTGGGCGCGCCCTAGCAGGGGCTCGACCTCGCCGAGCGGCGCGCTGTCGTGGCGCGGG								
H R L R E E T F G D P T P A G I V P E L E R L A A Q H R R P								
3420								
StuI								
↓								
GCGGCGCGACGCGCGGACCTGAGCGCGCACCCCTCGCCCCAGCGCTCACCCCTGTATCTGCGCCGGGGGACGCCCCCGGCCACCCCTCCGA								
CGGCGCGCTGCGGCGCGTGA CTGCGCGTGGGAGCGGGGTCCGGAGTGGGACATAGACGCGGCGCCCTCGCGGGGCGCGGTGGGAGGCT								
P A D A R H								
3510								
AatII								
↓								
AAAGACCGAAGAGGAGCACCGTGACGAAGTCGACCAAGCGCGACGCTACGACCTCTTCTACCTGGGTGCGGCAAGGACTACGCCGCGC								
TTCTGGCTTTCGTCCCTCGTGGCACATGCTTCAGCTGTTGCGGCTGCAGATGCTGGAGAAGATGGACCCAGCGCCGTTCTCTGATGCGGCGG								
V Y E V D H A D V Y D L F Y L G R G K D Y A A								
3600								
EarI								
↓								

FIG. 32J

[illegible]

GAGGCCCTCCGACATCGCCGACCTGGTGGCTCCCGTACCCCGAGGCCTCCTCGCTCTGGACGTGGCCTGCGGTACGGGCACGCATCTG
CTCCGGAGGCTGTAGCGGCTGACCA CGCGAGGGCATGGGGGCTCCGAGGAGCGAGGACCTGCACCGGACGCCCATGCCCGTGGGTAGAC
E A S D I A D L V R S R T P E A S S L L D V A C G T G T H L

GAGCACTTCAACCAAGGATTGGCGACACCGCCGGCCTGGAGCTGTCCGAGGACATGCTACCCACGCCCGCAAGCGGCTGCCCGACGCC
CTCGTGAAGTGGTTCTCAAGCCGCTGTGGCGGCGGACCTCGACAGGCTCCTGTACGAGTGGGTGCGGGCGGTTGCCCGACGGGCTGCGG
E H F T K E F G D T A G L E L S E D M L T H A R K R L P D A

ACGCTCCACCAAGGGCGACATCGGGACTTCGGGCTCGGCCGGGAAGTTCTCCGCCGCTGGTCAGCATGTTCAAGCTCCGTCGGCTACCTGAAG
TGGAGGTGGTCCCGCTGTACGCCCTGAAGGCCGAGCCGGCCCTTCAAGAGCGGGCACCAAGTCGTACAAGTCGAGCGCAGCCGATGGACTTC
T L H Q G D M R D F R R L G R K F S A V V S M F S S V G Y L K

ACGACCGAGGAATCGGCGGGCCGTCGCCTCGTTCCGGAGCACCTGGAGCCCGGTGGCGTCTGTCGTCGAGCCGTGGTGGTTCCCCG
TGCTGGCTCTTGAGCCGCGCCGGCAGCGGAGCAAGCGCTCGTGGACCTCGGGCCACCGCAGCAGCAGCAGCTCGGCACCAAGGGC
T T E E L G A A V A S F A E H L E P G G V V V E P W F P

FIG. 32K

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[illegible]

AatII DraIII
 ▼ ▼
 GAGACCTTCGCCGACGGCTGGGTCAAGCCGACGTCGTCCGCCGTACCGGGCGCACCGTGGCCCGTGTCTCGCACTCGGTGCGGGAGGGG
 CTCTGGAAGCGGCTGCCGACCCAGTCGGCGGTGCAGCAGGGGGCACTGCCCGCTGGCACCGGGCACAGAGCGTGAGCCACGCCCTCCCC
 E T F A D G W V S A D V V R R R D G R T V A R V S H S V R E G

AatII
▼
AAACGCGACGGCATGGAGGTCACCTTACCGTGGCCGACCCGGGCAAGGGCGTGCGGCATCTCTCCGACGTCCTCATCACCCCTGTTT
TTGCGGTGCGCGTACCTCCAGGTGAAGTGGCACCCGGCTGGGCCCGGTTCCCGCACGCCGTGAAGAGGCTGCAGGTAGTAGTGGGACAAG
N A T R M E V H F T V A D P G K G V R H F S D V H L I T L F

SfiI EarlI
 ▼ ▼
 CAC CAG GCC AGT AC GAG GCC GGT TCA CGG CCC CGG GCT CG AGT ACC TGG AGG GCG GCC CGT CGG CCT CT TCG TC
 H Q A E Y E A A F T A A G L R A V E Y L E G G P S G R G L F
 4230

[illegible]

FIG. 32L

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sugar.finalgene b-1 Sequence

10 20 30 40 50 60 70 80 90
1234567890123456789012345678901234567890123456789012345678901234567890

NotI
▼

AAGACCCGAATACCGCGTGTCCGCGCGCGCCGACACGCCCCAGGGCCCTTCAACCCTGGCCCGTCTGGCACCCCTGCTGGCGGGCACCACC
TTCCTGGGCTTATGGCGCACAGGCGCGCGCGCGTGGTGGGAGTCCGGAACTGGGACCGGCAGCAGCCGCTGGGACGACCGCCCGTGGTGG
K T R I P R V R R G R T T P R A F T L A V V G T L L A G T T 4410

NotI
▼

GTGGCGCGCGCGCTCCGCGCGCGCCGACACGGCCCAATGTTCACTACACGAGCCGGCGGGAGCTCGTCGCCACAGATGACGCTCGAC
CACCGCGCGCGAGGCGCGCGCGCTGTGCCGGTTACAAGTCACTGTGCTCGGCCCGCCCTCGAGCAGCGGGTCTACTGCGAGCTG
V A A A P G A A D T A N V Q Y T S R A A E L V A Q M T L D 4500

GAGAAGATCAGCTTCGTCCACTGGGCGCTGGACCCCGACCGGCAGAACGTCGGCTACCTTCCCGCGGTGCGCGCTCTGGGCATCCCGGAG
CTCTTCTAGTCGAAGCAGGTGACCCCGGACCTGGGGCTGGCCGCTCTTGACGCCGATGGAAAGGCGCGCACGCGGTAGGGCCTC
E K I S F V H W A L D P D R Q N V G Y L P G V P R L G I P E 4590

MscI
BclI
▼

CTGCGTCCGCGCGACGGCCGAAACGGCATCCGCGCTGGTGGGCGAGACCGCCACCGCGCTGCCCGCGCGGTGCGCCCTGGCCAGCACCTTC
GACGCACGGCGGCTGCCGGCTTGCCTAGGCGGACCAACCCGCTGTGGCGGTGGCGCGACCGGCGCGCGGACCGGTGCGTGAAG
L R A A D G P N G I R L V G Q T A T A L P A P V A L A S T F 4680

FIG. 32M

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
123456789012345678901234567890123456789012345678901234567890								
<div> <div> <div>Styl</div> <div>NcoI</div> <div>▼</div> </div> <div> <div>PflMI</div> <div>▼</div> </div> <div> <div>Apal</div> <div>▼</div> </div> </div>								
GACGACACCATGGCCGACAGCTACGGCAAGT	CATGGCGCGGACGGTCGGCGCTCAACCAGGACATGGT	CCTGGGCCCGATGAAC	4770					
CTGCTGTGGTACCGGCTGTCCAGTACCGCGCTGCCAGCGCGAGTTGGTCTGTAC	CAGGACCCGGCTACTACTTG							
D D T M A D S Y G K V M G R D G R A L N Q D M V L G P M M N								
<div> <div> <div>Styl</div> <div>NcoI</div> <div>▼</div> </div> <div> <div>PflMI</div> <div>▼</div> </div> <div> <div>Apal</div> <div>▼</div> </div> </div>								
AACATCCGGGTCCGACGGCGCGGAACTACGAGACCTT	CAGGAGACCCCTGGTCTCCTCGCGCACCGCGGTGCCCCAGATCAAG	4860						
TTGTAGGCCCCACGGCGTGC	CGCGCCTTGATGCTCTGGAAGTCGCTCCTGGGGACCAAGAGAGCGCGTGGCGCCAGCGGGTCTAGTTC							
N N I R V P H G G R N Y E T F S E D P L V S S R T A V A Q I K								
<div> <div> <div>Styl</div> <div>NcoI</div> <div>▼</div> </div> <div> <div>PflMI</div> <div>▼</div> </div> <div> <div>Apal</div> <div>▼</div> </div> </div>								
GGCATCCAGGTGCGGTCTGATGACCA	CGGCCAAGCACTTCGGGCCAACAACCAAGGAGAACACCGCTTCTCCGTGAACGCCAATGTC	4950						
CCGTAGGTCCACGCCCAGACTACTGGTGCCGGTT	CGTGAAGCGCCGGTTGTTGGTCTCTTGTGGCGAAGAGGCACCTTGGCGTTACAG							
G I Q G A G L M T T A K H F A A N N Q E N N R R F S V N A N V								
<div> <div> <div>Styl</div> <div>NcoI</div> <div>▼</div> </div> <div> <div>PflMI</div> <div>▼</div> </div> <div> <div>Apal</div> <div>▼</div> </div> </div>								
GACGAGCAGACGCTCCGCGAGATCGAGTCCCGCGGTTCGAGGCGTCTCCAAGCCCGCGCGCTCCTT	CATGTGTGCTTACACGGC	5040						
CTGCTCGTCTCGAGGCGCTCTAGCTCAAGGGCCGCAAGCTCCG	CAGGAGTTCGGCCCGCGGAGGAGTACACACGGATGTTGCCG							
D E Q T L R E I E F P A F E A S S K A G A A S F M C A Y N G								

FIG. 32N

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sugar.finalgene b-1 Sequence

[illegible]

FspI DraIII
 ▼ ▼
 CTCAACGGGAAGCCGTCTCTGCGGCAACGACGAGTCTCTCAACAACGTCTGCGCACGAGTGGGGCTTCCAGGGCTGGGTGATGTCCGAC
 GAGTTGCCCTTCGGCAGGACGCCGTTGCTGTCTCAGGAGATTGTCACGACGCGTGCCTACCCCGAAGTCCCGACCCACTACAGGCTG
 L N G K P S C G N D E L L N N V L R T Q W G F Q G W V M S D

StyI EcoNI PflMI AatII
 ▼ ▼ ▼ ▼
 TGGCTCGCCACCCGGGCAACGACCCATCACCAAGGGCCTCGACCAGAGATGGGGCTCGAGCTCCCGGGCGACGTCCCGAAGGGCGAG
 ACCGAGCGGTGGGGCCCGTGGCTGCGGTAGTGTTCCGGAGCTGGTCTCTTACCCGACGCTCGAGGGGGCCGCTGCAGGGCTTCCCGCTC
 W L A T P G T D A I T K G L D Q E M G V E L P G D V P K G E

BsaI
▼
CCCTCGCCGCGGCCAAAGTTCTTCGGCGAGGCGCTGAAGACGGCCCGTCTGAACGGCACGGTCCCGAGGCGGCCGTGACGCGGTCTGGCG
GGGAGCGGCGGCCGGTTCAGAAAGCCGCTCCGCGACTTCTGCGCGCAGGACTTGTCCGTCCAGGGGCTCCGCCGCGCACTGCCGCCAGCCGC
P S P P A K F F G E A L K T A V L N G T V P E A A V T R S A

GAGCGGATCGTCGGCCAGATGGAGAAGTTCGGTCTGCTCCTCGCCACTCCGGCGCGCGCGGCCCGGAGCGCGGACAAAGCGGGTGCCCCAGGCG
CTCGCCTAGACGCCGGTCTACCTCTTCAAGCCAGACGAGCGGTGAGGCGCGCGCGCGCGCGCGCTCGGCTGTTCGGCCACCGGGTCCGC
E R I V G Q M E K F G L L A T P A P R P E R D K A G A Q A

FIG. 320

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[illegible]

FspI **AlwNI**

GTGTCCCGCAAGGTCGCCGAGAACGGCGCGGTCTCTCTGCGCAACGAGGGCCAGGCCCTGCCGCTCGCCGGTGACGCCGGCAAGACATC
CACAGGGCGTTCACGGGCTCTTGTCCGCGGCCACGAGGACGGCTTGTCTCCCGTCCGGACGGCGAGCGGCCACTCGCGCCGTTCTCTGTAG
V S R K V A E N G A V L L R N E G Q A L P L A G D A G K S I

BstEII
StyI ▼

5580
GCGGTCAATCGGGCCCGACGGCCCGTCGACCCCAAGTCAACCGGCCCTGGGCAGCGGCCACAGTCGTCCCGGACTCGGGCGGGCCCACTCGAC
CGCCAGTAGCCGGGCTGCCGGCAGCTGGGGTTCAGTGGCCGACCCGTTCGGGGTGCAGCAGGCCCTGAGCCGCCCGCGGTGAGCTG
A V I G P T A V D P K V T G L G S A H V V P D S A A P L D

5670
ACCATCAAGCCCGCGGGTGCGGTACGTACGAGACGGGTGAGGAGACCTTCGGACGCGAGATCCCGCGGGGAACCTC
TGGTAGTTCGCGGGCGGCCACGCCACGCTGCCACTGCTCTGCCACTCTCTGGAAGCCCTCGGTCTAGGGCCGCCCTTGGAG
T I K A R A G A G A T V T Y E T G E E T F G T Q I P A G N L

XhoI
PaeRI

AGCCCGGGCTTCAACAGGGCCACCAGCTCGAGCCGGGCAAGGGGGGGCGCTGTACGACGGCACGCTGACCGTGCCCCCGCCGACGGCGAG
TCGGGGCCGCAAGTTGGTCCGGTGGTTCGAGCTCGGCCCGCTCCGCCCGCGACATGCTGCCGTGCGACTGGCACGGGGCGGTGCCGCTC
S P A F N Q G H Q L E P G K A G A L Y D G T L T V P A D G E

FIG. 32P

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[illegible]

RsrII AgeI
 ▼ ▼
 TACCGCATCGCGGTCCGTGCCACCGGTGGTTACGCCACGGTGCAGTCCGGCAGCCACACCATCGAGGCCGTGAGTCTACGGCAAGGTG
 ATGGCGTAGCGCCAGGCACGGTGGCCACCAATGCGTGCCACGTTCGAGCGTGGTGTGGTAGTCTCGGCCACGTCCAGATGCCGTTCCAC
 Y R I A V R A T G G Y A T V Q L G S H T I E A G Q V Y G K V

5850

styl ▼ NruI ▼
 AGCAGCCCGTCTCAAGCTGACCAAGGGCAGCACCAAGCTCAGATCTCGGGCTTCGGCGATGAGTGCCACCCCGCTCTCCCTGGAGCTG
 TCGTCGGGCGAGGAGTTCGACTGGTTCCTCGTGGTTCGAGTGTAGAGCCCGAAGCGCTACTACGGTGGGCGGAGAGGACCTCGAC
 SSSPILLKLLTKLTKGTHKLLTISGFAMSA TP L S L E L

NruI
 PvuI
 BbsI
 6030

GAGGACGGCA CCGAGGGCGTCGACCGTCCGAACCTGTGCTGCCGGGTACGCAGGACAAGCTGATCTCGGCTGTGCGCGGACGCCAACCCG
CTGCTGCCGTGGCTCCCGCAGCTGGCAGGCTTGGACAGCGACGGCCCATGCGTCTGTTCGACTAGAGCCGACAGCGCTGCGGTGGGC
D D G T E G V D R P N L S L P G T Q D K L I S A V A D A N P

FIG. 32Q

FIG. 32R

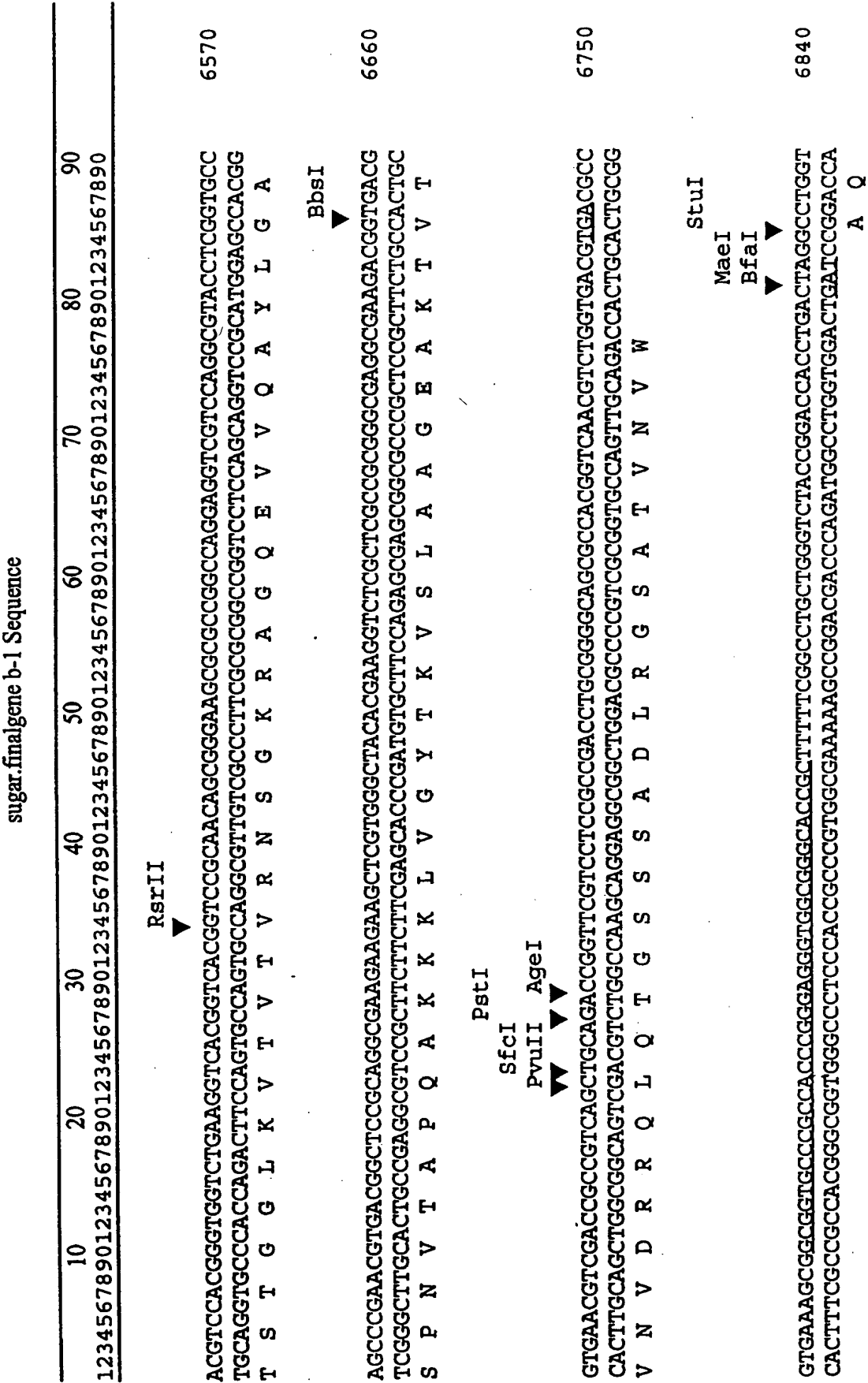


FIG. 32S

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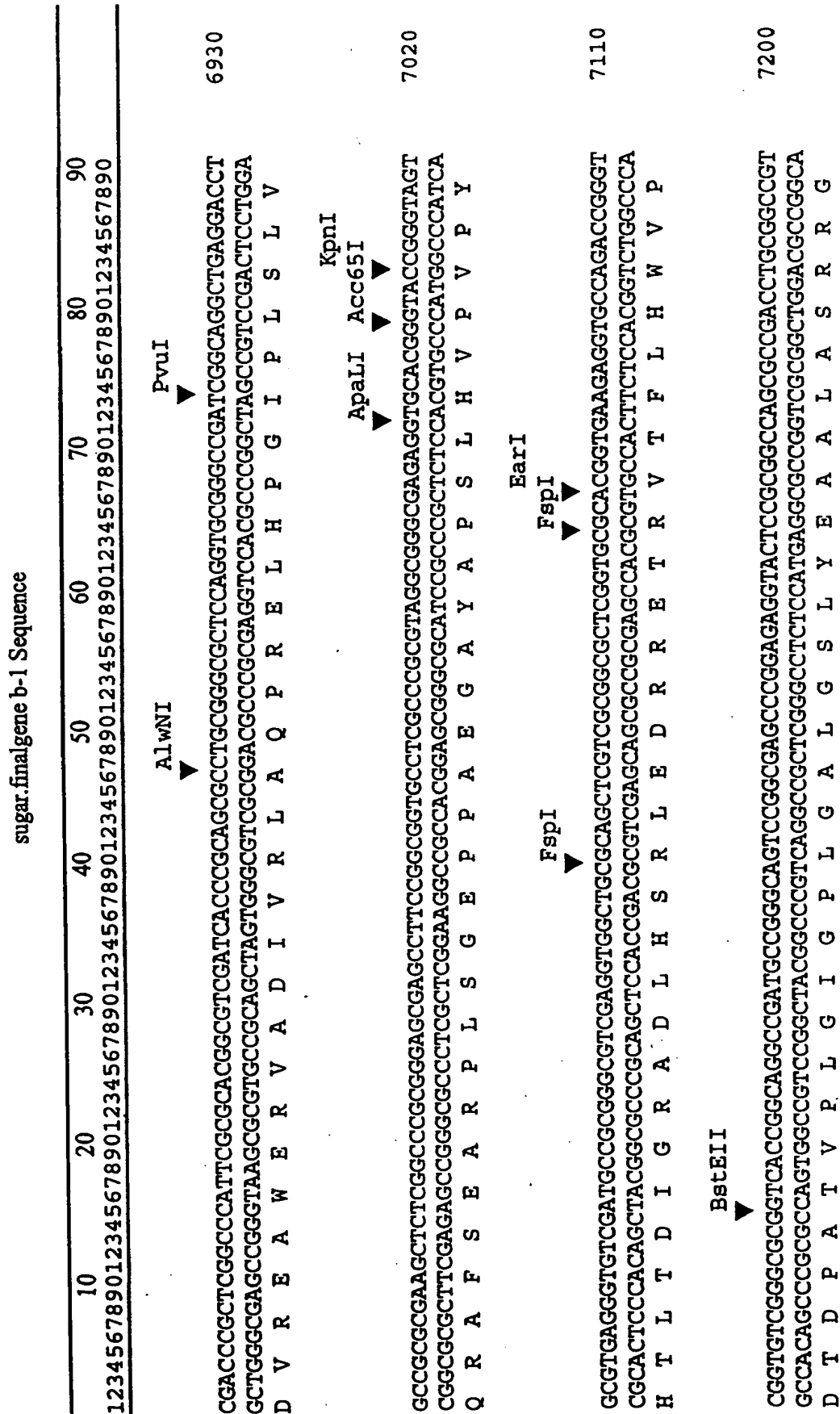


FIG. 32T

	10	20	30	40	50	60	70	80	90
123456789012345678901234567890123456789012345678901234567890									
PvuII	BamHI	XcmI							
▼	▼	▼							
TCCAGCTGTCCAGTGGGCGGACCGGATCCGCAGCACGGCGGCCCTGCATCTCGTCCAGGCGGAGTTGGTGCCCTTCGTCTCGTGGCTGT									7290
AGGTTCGACAGGTCCACCCGCTCGGCTTAGGGCTGTGTCGCCCGGACGTAGAGCAGGTCCGCCCTCAACCACGGGAAGCAGACCCGACA									
NWSDLLHALRLRI RLVAQAQME DLR SN T G K T E H S									
BspMII									
BspEI									
▼									
ACTTCTGCCGCGAGCCGTAGTTGCGGAGCATCCGGAGCCGTTCCGGGAGCTCGGGTCCCGGTGACGACGGCGCCCGCGTCGCCGAAGC									7380
TGAAGACGGCGCTCGGCATCAACGCTCGTAGGCCTCGGCAAGCCGCTCGAGCCCCAGCGGCCACTGTCGCCGCGGCGGACGCGCTCG									
YKQRSSGYNRLMLRLEAL EPD GT V V A G G D G F									
AGCCGAGTTCTTGCCCGGTAGAAGCTGAACGGGGCCACCGACGACCCGGCGCCGATCCGCCGGCCCCGGTAGCGGGCGCCGTGGGCCT									7470
TCGGCTCCAAGAACGGGGCCATCTTCGACTTGCGCCGTTGGTCTGCTGGCGCGGCTAGGCGGCGCGGGGCCATCGCCCGCGGCACCCGGA									
CGLNKGP YFSFAAVSSSG AG I R R G R Y R A G H A									
RsrII									
▼									
GCGCGGCTCTCGACGATGTGAGGCCGTGCCGCTCCGCGAGCTCGCGGAGGGCGTCCATGTCCGCGGGGTGCCCGTAGAGTGGACGG									7560
CGCGCCGCGAGAGTGTACAGTCCGGCACGGCCAGGCGCTCGAGCGCTCCCGCAGGTACAGCCGCCCCACGGGCATCTCCACCTGCC									
QAADEVIHLGLGHRRDALERLADMDAPHG Y L H V									

FIG. 32U

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
123456789012345678901234567890123456789012345678901234567890								

GGAGGAGCGCCCGGCTGCGGGGGTGATCGCCTTCTCGACGAGCAGCGGGTCCAGGGTGGGGTGGTCTCGTGGGCTCGACGGGCAAGG
CCTCCTCGCGGGCCACGCCCCCCTAGCGGAAGAGCTGCTCGCCAGGTCCACCCACAGGAGCACGCCGAGCTGCCGTGCC
P L L A R T R P T I A K E V L L P D L T P H D E H P E V P V 7650

BsaAI
AflIII
PvuII

GGTTCGCGCGGTGGCGGACACCGGAGCCAGCTGGCGATGTACGTGTCGAGGGGACGATCACCTCGTCCCCTGGGTCCGATGCCGAGGC
CCCAGCGGGCCACCGCCTGTGGCGCTCGGTGACCGCTACATGCACGCTCCCTGTCTAGTGAGCAGGGGCCAGGCTACGGCTCCG
P T A G T A S V A L W S A I Y T H S P V I V E D G P G I G L 7740

TfII

CGCGGAGGGCGAGCTGGAGGGGTCCATCCCGTGTTCACGCCGACGGCGTGGTCCGTCTCGCAGTACGCGGCGAACTCCGCCCTCGAATC
GCGCCTCCCGCTCGACCTCCCGCAGGTAGGGCGACAAGTGGCGTCCCGCACCGAGCAGCGTATCGCCCGCTTGAGCGGAGCTTAG
G R L A L Q L A D M G S N V G V A H D T E C Y A A F E A E F 7830

PvuI

CTTCGAGTTCGGGTCCGAGGAGGTAGCGCCCCGAGTTCGAGGACGCGGGCGATCGCGCGTCTCGCGCGGAGCTCCTCGTAGGCGG
GAAGCTCAAGCCCCAGGCTCCTCCATCGCGGGGCTCAGCTCCTGCGCCCGTAGCGCCGAGCCAGAGCGCGCTCGAGGAGCATCCGCC
G E L E P G L L Y R G S D L V R A I A A D T E A R L E E Y A 7920

FIG. 32V

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[illegible]

BstXI PvuII
 ▼ ▼
 CCTTGAGGTCGAGGAAGGGGACGCGGGGTCTCGCGCGGCTCTCAGCGGACACCTCCAGCGGGTGGCGGCAGCTCGGGGCGGT
 GGAACCTCCAGCTCCTTCCCTGCGCCGCCAGAGCCGCGCCGACGAGTGGCTGTGGAGGTGCGCGCCACCGCCCGTCTGACGCCCCGCCA
 A K L D L F P V R P T E A R S S V A S V E V A T A P L Q P A T

KpnI
 Acc65I RsrII
 ▼ ▼
 CGCCTTGAGCGGCTCCACACAGCCGCGTCTCCCGGTACACAGCGGACGGTCCGCGCGAGGCCGTCCGCGAAGAGACCTCGGGCGGTA
 GCGGAACCTCGCCGAGGGTGGTCGGCGCCCAAGAGGGCCATGGTGCCTGCCAGGCGCGCTCCGGCAGGCGCTTCTCTGGACGCCCGCCAT
 A K L P E W G R N E R Y W R V T R A L G D A F S V Q P R Y
 RsrII

RsrII
 BspMII
 BspEI

▼ ▼

GCGGAGCTCGCGCTCGATCTGCGCCCGCTCGAGGGAGTAGCGCAGGTCGTGGCCCTTGCGTCCGGACCGAGGACCAGTC
 CGGCTCGAGCGCGAGCTAGAGCGGGCGGAGCTCCCTCATCGCGTCCAGCACCGGGAACGCCAGCCGCTGGAAGCCCTGGCTCCTGGTCAG

8190

G L E R E I E G G D L S Y R L D H G K R D A V K R V S S W D

BglII
▼
GGCGCCGAGCGAGTCCAGGAGGATGCCGGTGGTCAGCTCCAGGCCGCCCGATGTGGTAGATCTCGCCGGCCCGGCC
CCGGGCTCGCTCAGGTCTCTACGGCCACTCAAGGCCAACCAAGTCGAGTCCGGCGGGCTACACCATCTAGAGCGGCCGGCGCGG
A G L S D L L I G T L E R N T L E L G G I H Y I E G A R G

FIG. 32W

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
G C C C G G A G A C G A G C G G A T G C C C C G G C A G T G G T C G G T G T G C A C C C A C T C G C G G A C G T T C G C C C G T C G C C G T A C A G C G G A G C G T								
C G G C G C T C C T G C T C G C G T A C G G G C C G T C A C A G C A G C C A C A C G T G G T G A G C C C T G C A A G C G C G G C A G C G G C A T G T C G C C C T C G C A								
G A L V L A I G R C H D D T H V W E R V N A G D G Y L P L T								
C C C G C C G T C G A G A G T T C G T C A C G A A G A G G G G A T G A G C T T C T C G G G G T G C T G G T A C G G C C C G T A G T T G T T G C A G C A G C G G T G A T C C G								
G G G C G C A G C T C C T C C A A G C A G T G C T T C C C C C T A C T C G A A G A G C C C C A C G A C C A T G C C G G G C A T C A A C A C G T C G T C G C C C A C T A G G C								
G G D L L N T V F L P I L K E P H Q Y P G Y N N C C R T I R								
T A C G T C G A G G C C G T A C G T C C G G T G G T A G C C G G G G C A A C G A G T C G G A G C C G G C C T T G G A C G C C C G T A G G G C G A G T T G G G C T C C A G C G G								
A T G C A G C T C C G G C A T G C A G G C C A C C A T C C G G C C C G T T G C T C C A G C C T C G G C C G G A A C C T G C G G C G C A T C C C G C T C A A C C C G A G G T C G C C								
V D L G Y T R R H Y A R A V L D S G A K S A A Y P S N P E L P								
G C T G C T C G G T C C A G A G C C G G A G T C G A T C G A C C C G T A C A C C T C G T C G G T G G A G A C G T G C A C G A C C C G G C C G A C G C C G G C G T C G A C G G C								
C G A C G A G A G C C A G G T C C T C G G C C T C A G C T A G T G G C A T G T G A G A G C C A C C T C T G C A C G T G C T G G G C C G G C T G C G C C G C A G C T G C C G								
S S E T W S G S D I S G Y V E D T S V H V V R G V G A D V A								

FIG. 32X

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[illegible]

AlwNI
 ▼
 Pml I
 BsaAI
 ▼
 8730

CCQLLTQTGTGVNTETFVSA.GAISR DVHSEAA

GAAGTGAAGATGGCGTCCAGCCGCGCAGTTCCCGGGCGAGGAGCCCGGCGTCGCGGATGTCCCGTGGACGAAGCGCAGTCGCGGGTC
CTTACCTGCTACCGCAGGTGCGGCGCGTCAAGGCGCGCTCCTCCGGCGCGCAGCGCCTACAGCGGCACCTGCTTCGCGTCAGCGCCCGAG

F H V I A D V G R L E R A L L G A D R I D G H V F R L R P D D

CGCGTCCACCGGGCGAGGTTGGCGCGGTTGCCCGGTAAGTGAGGCTGTCCAGGACGATCACCTCATCGGGCGGCACGTCTGGGGTACGC
GCGCAGGTGGCCCGCGCTCCAACCGGCCCAACGGGCGCATCCACTCCGACAGGTCTGCTAGTGGAGTAGCGGCCCGGTGCAGGCCCATGGC

A D V P A L N A R R N G A Y T L S D L V I V E D A P V D P Y A

DraIII BstEII BbsI
 ▼ ▼ ▼
 CCCGGCGAGGAGCTGCCACGAAGTGCAGCCGATGAAGCCCGCACCTCCGGTCAACAGAAGCCGCACTGCCGTCTTCTTTCCGTGCGC
 GGGCCCGCTCCTCGACGGCGTGTTCACGCTCGGCTACTTTCGGGGCTGGAGGCCAGTGGTCTTCGGCGTGCAGCGCAGAAAGCAAGCCAGCG
 9000

G A L L O R V F H S G I F G A G G T V L L R V

FIG. 32Y

	10	20	30	40	50	60	70	80	90
123456789012345678901234567890123456789012345678901234567890									
SfCI									
MluI									
AflIII									
▼									
GCTGAGTCCGGGTGTGGTCGCACACTGTTCGGTGCGGGTCCGGTGTGGTTCGCACTGTTCGGTGGCGCTGTCCGTTCGTGGGAAC									9090
CGACATCCAGGCCACACCAGCGTGACAGCCACCGCCACGCCACGCCAGCCACACCCAGCGTGACAGCACCGCGACAGCCAGCACCCCTTG									
BsaBI									
StuI									
▼									
CGGTCCGGCCGAGGTGCCCTCAGGGGCTCCCTCGCGGCCGCGCATCTCCATCAGATAGTCCCGTACTCAGTTCGGTCCGGAGAGGCCTTCT									9180
CGCAGCCGGCGCTCCACGGGAGTCCCCGAGGGAGCGCCGCGCTAGAGGTAGTCTATCGACGGCATGAGCCACGCCCTCTCCGGAAGA									
P A G E R G A I E M L Y S G Y E T R S L G E									
StuI									
▼									
CCCAGGCCGTGACAGGCTTCGGCGTCGATGAAGCCCATGCCGAAGCGATCTCCTCAAGGCCCGCATCCAGACGCCCTGCCCGCTCCTCC									9270
GGTCCGGCACGTCCGGAGCCGAGCTACTTCGGGTACGCCTTCGCTAGAGGAGTTCCGGCGCTAGGTCTGCGGGACGGCGAGGAGG									
G L G H C A E A D I F G M R F A I E E L G A I W V G Q R E E									
PfIMI									
AlwNI									
▼									
AGGACCTGGACGTACTGGGCGGCCCGCAGGAGCGAGTCTGTGGTGCCGGTGTCCAGCCAGGCGAAGCCGGGCCAGGTTGACGAGTTCG									9360
TCTTGGACCTGCATGACCCCGCGGGCGTCCCTCGCTCAGCACCCACGSCCAGGTTCGGTCCGCTTCGGCGCCGGGTCCAAC TGCTCAAGC									
L V Q V Y Q A A R L L S D H T G T D L W A F G R G L N V L E									

FIG. 32Z

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sugar.flnalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
AatII								
▼								
GCCCGCCCGCTCAGGTAGACGCGGTTGACGTCGGTGATCTCCAGCTCGCCGCGCGGCGAGGGCCGGATGTTCTTGGCGATGTCGACG								9450
CGGGCCGGGCGAGTCCATCTGCGCCAACTGCAGCCACTAGAGTTCGAGCGGCGCGCTCCCGGCTACAAGAACCGCTACAGCTGC								
A R G R E L Y V R N V D T I E L E G R P S P R I N K A I D V								
AatII								
▼								
ACGTCGTTGTCGTAGAGGTAGAGCGCGGTGACGGCGAGGTTGGAGCGCGCTTGACGGGCTTCTCGACGAGGTCGGTCAGCCGCGCCCGTC								9540
TGCAGCAACAGCATCTCCATCTCCGGCCACTGCCGCTCCAACCTCGCGCCGAACTGCCGAGCTGCTCCAGCCAGTCGGCCCGGGCAG								
V D N D Y L Y L G T V A L N S R P K V P K E V L D T L R G T								
EaeI								
▼								
GCGTCCACCTCGGCGACGCCGTACCGCTCGGGTCTTGTGACCGGGTAGCCGGAAGACACGACGCCCTCGAGGCGCGGATGCTGTCCCGC								9630
CGCAGGTGGAGCCGCTGCGGCATGGCGAGCCCCAGGAACCTGGCCCATCGGCTTCTCGTGCGTCCGCGAGCTCCGCGCGCTACGACAGGGCG								
A D V E A V G Y R E P D K V P Y G F L V C G D L R A I S D R								
ApaI								
▼								
AGGAGCGTGTAGAGCGCGGCCCGTGGGAAGATGTTGTGCGCCAGGATCAGGGCGCAGGTGTGTCGCCGATGTGCTCGGCTCCGACGAGA								9720
TCCTCGCACATCTCCGGCCCGGCACCTTCTACAACAGCGGGTCCCTAGTCCCGGTCACAGCGGCTACACGAGCCGAGGCTGCTCT								
L L T Y L G P G H F I N D G L I L A C T D D G I H E A G V L								

FIG. 32AA

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
TfII								
▼								
AGTGGTCCGCGATTCTCTGGGCTCTTCTGGACCGCATAGTCGAGTTCTATTCACAGTGCCCTGCCGTTTCCGAGAACGCACTGGAAG								9810
TCACGCGAGCGCTAAGGACGCCCGAGAAAGACCTGGCGTATCAGCTCAAGATAAGGGTCCACGACGGCAAGGCTCTTCGCTGACCTTC								
L A D A I G A P E K Q V A Y D L E I G L H R G N G L L S Q F								
TfII								
▼								
TfII								
BsaBI NruI								
▼								
AGTTCGATGTCTGGGGTCTGAGATGATTTGAATCTCGGAATACCGCGAGCATGAGAACCGACGCGGATAGATCATCGGTTTG								9900
TCAAGCTACAGACCCCCAGCTCTACTAAACTTAGAGCGCTTATGGCGGCTCGTACTCTTGGCTGTGCGCTATCATCTAGTAGCCAAAC								
L E I H Q P T S I I Q I E R I G G L M L V S L P Y Y I M P K								
TfII								
▼								
TfII								
BstBI								
▼								
TTGTAGACCGGAAGAAATCTGCTTCGAAATGACCGAGGTCCCGGATGCAGCCGAGTTCGGCTCCCGCGCCAGGACTATTCCCTTCATT								9990
AACATCTGGCCTTCTAGACGAAGCTTTACTGGCTCCAGCGGCTACGTGGCTCAAGGCGAGGGCGGCGGCTCCTGATAAGGGAAGTAA								
N Y V P L I Q K S I V S T A P H L R T G S G A L V I G K M								
MaeI								
BfaI								
▼								
MaeI								
BfaI								
▼								
CTCGGAAACTAGCAGCAGGGCGCGGTGATAACGGTCGGCGTGGCGAGTTAGGGGGGCTAGGGGCTGCGCAGGGGAGTGTACCCACC								10080
GAGCCTTTGATCGTCCCGCGGCCACTATTGCCAGCCGACCGCTCAATCCCCCGCGATCCCGACGCGTCCCCCTCACAGTGGTGG								

FIG. 32BB

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
<div>BstXI</div> <div>▼</div>								
<div> Bsu36I</div> <div> ▼</div>								
<div> ApaI</div> <div> ▼</div>								
CCTTTGGGGGTGGGAAACACCGAGGGCCCGCGGACGGCCGGCCCTCAGGTGGGGGGATCGTGGGGGGGGATCGGGGGGATCGGG								
GGAAACCCCCACCTTTTGTGGCTCCCGGCCGGCCCTGCCGCCCGGGAGTCCACCCCTAGCACCCCTAGCCCCCTAGCCCCCTAGCCCC								
10170								
<div>PvuII</div> <div>▼</div>								
GCGGTGCGGGTCAGCGCAGGAAGCCGCGGGCCCTCTCCAGCCGTCGCGGGCTCGCGCTCCAGCTGGTTTCAGGCGGGCGGTGACGACC								
CGCCACGCCCCAGTCGCGTCTTCGGCGCCCGGAGGGTCCGCGAGGCGCGGCGCGAGGTCCGACCAAGTCCGCCCCCGCCACTGCTGG								
R L F G R A E E W G D A A D R E L Q N L R A T V V								
10260								
<div>ScaI</div> <div>▼</div>								
TGATCGAAGCCGTCATGAAGTACTCGTCGCCGTCGACGGCCGCCACCTCGCCGCCGCGCTCGACGAAGTCCCTGACGACCTCGGTGAGG								
ACTAGCTTCGGCAGGTACTTCATGAGCAGCGGCAGCTCCCGCGGTGGAGCGGCGCGGAGCTGCTTCAGGGACTGCTGGAGCCACTCC								
Q D F G D M F Y E D G D V A A V E G G R E V F D R V V E T L								
10350								
<div>EcoNI</div> <div>▼</div>								
GAGGTGTCGGGGTCAAGCGGCCCGCGATGTAGCGGTGCGGCCGTCCAGTCCGGGAAGCCGGCTCGCGGTACAGGTACACGTCGCGG								
CTCCACAGCCCCAGTGCAGCGCGCGGTACATCGCCCCAGCGCGGCGAGTCCAGCCCCCTTCGGCCGGAGCGCCATGTCCATGTGCAGCGGC								
S T D P T V R G A I Y R T A G D L D P F G A E R Y L Y V D G								
10440								
<div>AflIII</div> <div>▼</div>								

FIG. 32CC

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								

AGGAGATCGACCTGACCGGACCTGGGGTCCGGGTGGGGCCGATGGTGGGGGCTTGATCCGCAGCAGTTCCGGCGTCGGCCCCCGGTG
TCCTTAGCTGGACGTGGCGTGGACGCCACCGCGCCACCCGGCGTACCAACCGCCCGAAGTGGCGTCGTCAAGCCGAGCCCGGGGCCAC
L L D V Q V A V Q P H A T P R M T A P K I R L L E A D A G T 10530

FspI



CGCAGGCTGTTCAGGGCGTAGCCGTAGTCGATGTGGAGTCCGGGGTGGCTCGCGGACCCGCTCCTCGAAGCGTTGAGGGCCTCCTGG
GGTCCGACAAGTCCCGCATCGGCATCAGCTACACCTCAGGCCCCCAACCGGAGCGCCTGGCGAGGAGCTTCCGCAACTCCCGGAGGACC
R L S N L A Y G Y D I H L G P T R E R V R E E F A N L A E Q 10620

SfcI



NruI



PvuI



AGTCGGCCCCGCTCCTCCTCGCGGACGCTTGCCGTGTCACGGCCGCTGTAGTCCTCGCGAATGTTGACGAAGTCGATCGTCTGCCCTGC
TCGAGCCGGCGAGGAGGACGCCGTGGAACGGCAGCAGTGCCCGCGACATCAGGAGCGCTTACAACCTGCTTCAGCTAGCAGGACGGGACG
L E A R E E Q P L K G D D R G S Y D E R I N V F D I T R G Q 10710

CCGGCGTCGTTGAGTCGGCGATGAAGTCGACACGAGTCGAGCAGCGGGAGGACCGGCCCGGAGCAGCATGTAGCGGAAGCCGAGGTTG
GGCCCGCAGCAACTCCAGCCGCTACTTCAGCTGGTCCAGCTCGTCCGCCCTCCGTGCGGGCCCTCGTGCTACATCCGCTTCGGCTCCAAC
G A D N L D A I F D V L D L L R S A R G P L V I Y A F G L N 10800

FIG. 32DD

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sugar.finalgene b-1 Sequence									
10	20	30	40	50	60	70	80	90	
123456789012345678901234567890123456789012345678901234567890									
ATCGGCGACTCGCGCTCGGCGCGCAGCTGCTGGAAGCGGCGCAGGTTCTCGGGACGCGGCGGAAGGCGGCCTTCTTGCCGGTGGTCTGCTGC									
TAGCCGCTGAGCGCGAGCGCGCGTCCGACGACCTTCGCCGCGTCCAAAGAGCGCCTTGCGCCGCTTCCGCCGGAAGAACGGCCACCAAGACG									
I P S E R E A R L Q Q F R R R L N E R V R R F A A K K G T T Q									
10890									
TCGTACTCCTCGTTCGTTGAGCCCGTAGAGCGAGGTGCGGATGGCGTGCAGGCCCCAGAGGCCCGGGCTGGCGCTCCAGGGTGGCGTCCGGTG									
AGCATGAGGAGCAGCAACTCCGGCATCTCGCTCCACGCCTACCGCACGTCCGGGTCTCCGGCCCGACCGCGAGGTCCACCGCGAGCCAC									
E Y E E D N L G Y L S T R I A H L G W L G P Q R E L T R E T									
10980									
SfiI									
AGCGCGAAGGAGTTCGTGTAGACGGTGGGCCCGCAGCCCGTGGTGGTGGCGGCCAGGCTCCCGAGGCCGGGTTGGTGAGCGGC									
TCGCGCTTCCTCAAGCACATCTGCCACCCCGCGTCCGGCACCCAGCCACCGCACCGCCGGTCCGAGGGTCCGGCCCCCAACCACTCGCCG									
L A F S N T Y V T P R L G H D T A H A A L S G L G P N T L P									
11070									
TCCAGGCCCGGAGAGTACATCGCCGAGGGGTGCCCCGGGGTATCTCGTCGATGACCGACCGGAACATGGCGTTGCCGGCGTCGAGG									
AGGTCCGGGGCCTCTTCATGTAGCGGCTCCCCAACGGGCGCCCATAGAGCAGCTACTGGCTGGCCTTGTAACCGCAACGGCCGCGAGCTCC									
E L G G S F Y M A S P N G A P I E D I V S R F M A N G A D L									
11160									

FIG. 32EE

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sugar.finalgene b-1 Sequence

[illegible]

FIG. 32FF

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sugar.final gene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								

11610
 GGACAGAGCCCGCGCGGAGGGTCTGGCCGACGGCGGTGGACCGCCGCCCCAGATCGGCTCCGGGGTGGCGGACGCGTTCGGCCGGG
 CCGTGCTCCGGCGCGCCGCTCCAGACCGGCTGCCGACCTGGCGCGGGGTCTAGCCGAGGCCCCACGCGCGTCCGCAAGCCGGCCC
 P V L G G A A L T Q G V A H V A A G L D A G P H A C R E A P

11700
 GCGGTGGCGGAAGGCGGGCGGTCTCGGAGCGTCCAATCGTGGCGGTGGATGTCTGGGGGCCGCGAGCGGGGGGGGGCCGTGT
 CGCCACCGCCTTTCCCGCCCCCGCCAGTAGCCCTCGCAGGTAGCACCCCGCACCTACAGACCCCCCGCGCTGCCCCCGGGCACA
 A T A S L A P A T M R S R G I T P T S T Q P A A L P A P A T

NotI
 ▼

11790
 CGCGGTGGCGCGGTCAAGTTCGCGCGCGGGTTCGCGAGAGACGAGCGAGGTCCGGCGACCCGGCGGATGTCGTGCGCCGATGGCGG
 GCGCCACCGCGCGCAGTCAAGCGCGCGCGCGTCTCTGCGTCTGCGTCCAGCGCTGGCGCGCTACAGCAGCAGCGGCTACCGCC
 D R H R A T L E R G R T A C L R L L D A V R R I D D G I A

PflMI
 ▼

11880
 TGCCGTCGGCAGGACAGCAGCGCGCGGAGGGTTCGGTGTGGCGAGCGGGCGTGGCGTCCCGCGGTACGGCTCCAGCTCGT
 ACGGCCAGCCGTCCTGTCGTGCGCGCGCGCTCCGCAAGCCACACCGCTCGCCCCCGCACGCCGACGGGGGCCATGCCGAGGTCGAGCA
 T G T P L S L V R A A L R E T H P L P A H P Q G R Y P E L E

FIG. 32GG

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sugar.finalgene b-1 Sequence

10 20 30 40 50 60 70 80 90
 123456789012345678901234567890123456789012345678901234567890

▼
 ApaLI

GGCAGCCCGGAGAGTAGCGCGGGTGTGACGCCCTTCGGCTTCAGGACCTCCATGACGAGGTGCGGTGGATGCCGGTGGTGGCCT
 CCGTCGGCGCGCTCTTCATCCGCGCCACACGTGCGGAAGCCGGAAGTCTTGAGGTACTGCTCAGCGCCACCTACGGCCACCCACCGGA 11970

H C G P S F Y A R T H V G E A K L V E M V L D R H I G T T A

▼
 BsaAI

CGTCGATCTCGACGATCACGTACTGGTGGTTGTGAGCCCGTGGCGGTGCTGGCGACGAGGACGCGGGGAGGTCCGCGAGGTGCT
 GCAGCTAGAGCTGCTAGTCATGACCAACCAACTCCGGCACCGCCAGCACCGCTGCTCTGCGGCCCTCCAGGCGCTCCACGA 12060

E D I E V I V Y Q H N N L G H R D H D A V L V G P L D A L H

MluI
 AflIII
 ▼

StyI
 NcoI
 ▼

CGCGGTAGGCGCGTGGTTGCGCCGGTTCGGTTCGATGACCTCGGAAACGCGTCGAGGAGGTGAGGCCCATGGCGGCGGCGCTCGC
 GCGCCATCCGCGCACCAACGCGGCCAAGGCCAGCTACTGGAGCCCTTTGCGCAGCTCCCTCCACTCCGGGTACCGCCGCCCGGAGCG 12150

E R Y A A H N R R N R D I V E P F A D L S T L G M A A A E

▼
 BamHI

TCATCTTGGCGTTGGTCCCGCGGGGGTCCCGCGGGCAGGTGGAAGCCGAAGTTGTGAGGGCGCGGATCCGGCGGCGAGGTGCG
 AGTAGAACCGCAACAGGGCGGCGCGCCCGACGGCGGCGCTCCAGCTTCGGCTTCAACACCTCCCGCGCTAGGCCCGCGCTCCAGCC 12240

S M K A N T G G A P S G G P L D F G F N H L A R I R A A L D

FIG. 32HH

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sugar.final gene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
CGTCGTCGGTGACGACGGCGCGCCCTCGAAGGCGTTGACGGCCTTGGTGGCGTGAAGCTGAAGACCTCGGCGTCGCCGAGGCTGCCCGG								12330
GCAGCAGCCACTGTGCTGCCGCGCGGGAGCTTCCGCAACTGCCGGAACCAACCGCACCTTCGACTTCTGGAGCCGCGAGCGGCTCCGACGGCC								
A D D T V V A G G E F A N V A K T A H F S F V E A D G L S G								
CGGGCCGGCCGTCGACCGCGCAGCCGAGGGCGTGC GCGGCGTGAAGTACAGCCGAGGCGCGTGTCTGTCGGCGACCTTCCGCAAGCTGGT								12420
GCCCCGCGGAGCTGGCGCGTCCGCGACGCGCGCGAGCTTCATGTCTGGCGTCCGCGCACGAGCAGCCGCTGGAAGCGCTCGACCA								
A P R G D V A C G L A H A A D F Y L R L G H E D A V K R L Q								
CGGGCGCGCAGGGCGGCCCCAGAGGTGGACGCCGACGACGGCCGAGGTGCGGGGTGTGACCGCGCGGCCACCTGGTCCGGGTCCGAGGT								12510
GCCGCGCGTCCCCGCGCGGGTCTCCACCTGCGGCTGCTGCGGCTCCACGCCCCACACTGGCGCCGCGGTGGACCGAGGCCAGCTCCA								
D A A C P R G W L H V G V V A S T R P T V A A A V Q D P D L								
TGCCGGTGTCCGGGTGATGTTCGGCGAAGACCGGGGTGAGGCCGATCCAGCGCAGTGC GTGCGGGTGGCGGCGAAGCTCATCGACGGCA								12600
ACGGCCACAGGCCCCAGCTACAGCCGCTTCTGGCCCCCACTCCGGGTAGTTCGGTGCAGTCACGACGCCCCCACCGCCGCTTGCACTAGTGCCT								
N G T D D P D I D A F V P T L G I W R L A H P T A A F T M S P								

FIG. 32II

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
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M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G A A H A L L Q L G A T A N C T A V A H R V G								
M I V E G T L G								

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sugar.finalgene b-1 Sequence

10 20 30 40 50 60 70 80 90
123456789012345678901234567890123456789012345678901234567890

TGACGTACGACGAGATGGTCGATTGTGGTGGTGGGACTCTAATCCGCGCGGAACGGGACCGACAAGAGCACGCTATGCGC
ACTGCATGCTGCTCTACAGCTAACACACCAGCTAAAGCCCCCTGAGATTAGCGCGGCCCTTGCCCTGGCTGTTCTCGTGCATACGGC 13050

TCTCGATGTGCTTCGGATCACATCCGCCCTCCGGGGTATTCCATCGGGGCCCGAATGTGATGATCCTTGACAGGATCCGGGAATCAGCCG
AGAGCTACACGAAGCCTAGTGTAGCGGAGGCCCCCATAAGGTAGCCCGCGGCTTACACTACTAGGAACCTGCTCCTAGGCCCTTAGTTCGGC 13140

AGCCGCCGGAGGGCCGGCGCGCTCCGCGGAAGAGTACGTGTGAGAAAGTCCCGTTCCTCTCCCGTTTCCGTTCCGCTTCCGGCCCCG
TCGGCGGCCCTCCCGGCCCGCGGAGCGCCTTCTCATGCACACTCTTCAGGGCAAGGAGAAAGGCAAGGCAAGGCCGAGGCCGGGCC 13230

TCTGGAGTCTCCGTGCGCCGTACCAGCAGGGAACGACCGCTTCTCCCCCGGTACTCGACCTCGGGGCCCTGGGCAAGGATTTCCGGC
AGACCTCAAGAGGCACGCGGCATGGGTCCCTTGCTGGCGAAGAGGGGCCCATGAGCTGGAGCCCGGGACCCCGTCTCTAAAGCGCG
V R R T Q Q G T T A S P P V L D L G A L G Q D F A A 13320

FIG. 32KK

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sugar.finalgene b-1 Sequence

10	20	30	40	50	60	70	80	90
1234567890123456789012345678901234567890123456789012345678901234567890								